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(71) Applicant: THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK [US/US]; 116th Street and Broadway, New York, NY 10027 (US).

(72) Inventors: RZHETSKY, Andrey; 560 Riverside Drive, 11F, New York, NY 10027 (US). KALACHIKOV, Sergey; 154 Haven Avenue, 1303, New York, NY 10032 (US). KRAUTHAMMER, Michael, O.; 27 W. 76th Street, Apt. 3A, New York, NY 10023 (US). FRIEDMAN, Carol; 14 Dimitri Place, Larchmont, NY 10538 (US). KRA, Pauline; 109–14 Ascan Avenue, Forest Hills, NY 11375 (US).

(74) Agents: TANG, Henry et al.; Baker Botts LLP, 30 Rockefeller Plaza, New York, NY 10112–0228 (US).

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(54) Title: GENE DISCOVERY THROUGH COMPARISONS OF NETWORKS OF STRUCTURAL AND FUNCTIONAL RELATIONSHIPS AMONG KNOWN GENES AND PROTEINS

(57) Abstract

The present invention relates to methods for identifying novel genes comprising: (i) generating one or more specialized databases containing information on gene/protein structure, function and/or regulatory interactions; and (ii) searching the specialized databases for homology or for a particular motif and thereby identifying a putative novel gene of interest. The invention may further comprise performing simulation and hypothesis testing to identify or confirm that the putative gene is a novel gene of interest. The present invention also relates to natural language processing and extraction of relational information associated with genes and proteins that are found in genomics journal articles. To enable access to information in textual form, the natural language processing system of the present invention provides a method for extracting and structuring information found in the literature in a form appropriate for subsequent applications.

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GENE DISCOVERY THROUGH COMPARISONS OF NETWORKS OF STRUCTURAL AND FUNCTIONAL RELATIONSHIPS AMONG KNOWN GENES AND PROTEINS

SPECIFICATION

The invention described herein was funded in part by a grant from the National Library of Medicine, namely, Grant Number's LM06274 and LM05627. The United States Government may have certain rights to the invention. The present specification contains a computer program listing which appears as a microfiche Appendix H.

STATEMENT REGARDING MATERIAL SUBJECT TO COPYRIGHT

An appendix containing source code listing utilized in practicing an exemplary embodiment of the invention is included as part of the Specification.

1. INTRODUCTION

The present invention relates to methods for identifying novel genes comprising: (i) generating one or more specialized databases containing information on gene/protein structure, function and/or regulatory interactions; and (ii) searching the specialized databases for homology or for a particular motif and thereby identifying a putative novel gene of interest. The invention may further comprise performing simulation and hypothesis testing to identify or confirm that the putative gene is a novel gene of interest.

The present invention relates to natural language processing and extraction of relational information associated with genes and proteins that are found

in genomics journal articles. To enable access to information in textual form, the natural language processing system of the present invention provides a method for extracting and structuring information found in the literature in a form appropriate for subsequent applications. Specifically, the present invention provides for the generation of specialized databases containing information on gene/protein structure, function and regulatory interactions based on the retrieval of such information from research articles and databases, and computer representation of such information in a manner that allows efficient access to the extracted information.

The invention further provides for the use of the specialized databases for identifying novel genes based on detection of sequence similarities and domain/motif matches between genes/proteins, computation and interpretation of phylogenetic trees for multigene families, and analysis of homologous regulatory networks. The methods of the invention are based on the observation that functionally similar regulatory systems are generated during evolution by genetic duplication of ancestral genes. Thus, a comparison of homologous/similar networks within the same organism and between different species will allow the identification of genes absent in one of the systems under comparison. In this way genes that contribute to the phenotype of a specific disease associated with a particular biological system under analysis may be identified.

2. BACKGROUND OF THE INVENTION

2.1. NATURAL LANGUAGE PROCESSING

Researchers working in molecular biology must constantly consider the information present in the literature relating to their regulatory systems of interest and the genes and proteins that operate within those systems. Unfortunately, to remain up-to-date on the relevant literature, the researcher is required to perform laborious reading and manual integration of research articles, each of which may address a narrow subject. Therefore, technology that enables rapid retrieval of information from literature and manipulation of derived functional data should have a dramatic effect on the accesss of the researcher to important facts and ultimately should facilitate the discovery of novel human genes.

Natural language processing is an automated system that provides for a complex of programs for automatic retrieval of information from text analysis and for the computer representation of that information in a form that allows efficient access and extraction of that information. MedLee (Medical Language Extraction and Encoding System) has recently been successfully used for processing different types of medical texts as described in co-pending United States Patent Application Serial Number 09/370,329, incorporated herein in its entirety by reference (see also, Friedman et al., 1994, J. Amer. Med. Inf. Assoc. 1:161-174; Hripcsak et al. 1995, Ann. Intern. Med. 122:681-688; Hripcsak et al., 1998, Meth. Inform. Med.; Jain et al., 1996, Proc. AMIA Annu. Fall Symp. 542-546; Knirsch et al., 1998). When tested, MedLEE was on average as successful in retrieving reports associated with specified clinical connections as twelve medical experts invited for evaluation of the system.

Another text analysis technique has recently been developed that combines finite-state machines with statistical machine learning approaches. These models extract detailed semantic information from texts (e.g., see Hatzivassiloglou 1996, In Klavens, J.L., and Resnick, P.S. (eds) *The Balancing Act: Combining Symbolic and Statistical Approaches to Language*, MIT Press, Cambridge, MA) when extensive prior knowledge about the domain is not available. The techniques have been subsequently applied to the tasks of (i) automatically identifying medical terms for the automated summarization of research articles reporting on clinical studies and (ii) sanitizing sensitive information in patient records so that they can be widely disseminated for research purposes.

A number of projects have also been developed as statistical information extraction tools that operate with limited or no prior knowledge about the application domain. These earlier efforts include XTRACT, a tool that recovers collocational restrictions between words that has been licensed to more than thirty sites worldwide (Smadja, F., 1993, J. Comp. Ling. 19:143-177), CHAMPOLLION, a system that retrieves bilingual mappings between words and phrases in parallel texts from different languages (Smadja, F. et al. 1996, J. Computational Linguistics 22:1-38), and a system that automatically aligns noisy, semi-parallel texts from different languages (Fung, P. and McKeown, K.R., 1997, Machine Translation 11:23-29).

2.2. IDENTIFICATION OF NOVEL GENES

A variety of different methods are currently utilized for the identification and characterization of novel genes. Perhaps the most widely used method for generating large quantities of sequence information is via high throughput nucleotide sequencing of random DNA fragments. A disadvantage associated with this gene discovery technique is that in most instances when genes are identified their function is unknown.

For identification of specific disease genes, positional cloning is currently the most widely used method. The positional cloning approach combines methods of formal genetics, physical mapping and mutation analysis and usually starts with a precise description of the disease phenotype and a tracing of the disease through families of affected individuals. Genetic linkage data obtained from the analysis of affected families frequently allows the determination of an approximate genomic localization of the candidate disease gene with a precision of several millions of nucleotides. Once localized, the genetically defined chromosomal region is then recovered from genomic libraries as a contiguous set of genomic fragments. Genes residing in the disease-related region are determined by analysis of transcripts that are transcribed from the genomic fragment. From this analysis an initial set of candidate genes for a particular disease are identified based on the presence of the gene product in the biological system affected by disease and a correlation between its expression pattern and the pattern of disease progression.

Important information for selection of candidate genes also comes from analysis of their homology with genes known to be part of the same or related biological system. Finally, the ultimate proof of association between a gene and a genetic disorder comes from mutational analysis of a gene in patients affected by the disorder and from demonstration of a statistical correlation between occurrence of mutation and the disease phenotype.

Although positional cloning is a powerful method for gene discovery, the experimental method is extremely tedious and expensive. Moreover, disease genes implicated in genetically complex disorders, *i.e.*, those controlled by multiple

loci, can hardly be found using this strategy because of the complications associated with multiple loci linkage analysis.

Specialized databases for homology searches have also been utilized in disease gene discovery projects. In recent years a number of efficient sequence comparison tools have been developed such as the BLAST (Basic Local Alignment Search Tool) family of programs designed for comparison of a single "search sequence" with a database (see Altschul et al., 1990, J. Mol. Biol. 215:403-410; Altschul et al., 1997, Nucleic Acids Res. 25:3389-3402), the family of Hidden Markov Model methods for comparison of a set of aligned sequences that usually represent a protein motif or domain with a database (e.g., Krogh et al., 1994, J. Mol. Biol. 235:1501-1531; Grundy et al., 1997, Biochem Biophys. Res. Commun. 231:760-6) and various other comparison tools (Wu et al., 1996, Comput. Appl. Biosci 12:109-118; Neuwald et al., 1995, Protein Sci. 4:1618-1632; Neuwald, 1997, Nucleic Acids Res. 25:1665-1677).

When used in disease gene discovery projects, homology searches can be enhanced by creating specialized databases that utilize statistical analysis for evaluating significance of sequence similarities in comparison of new sequences with a database of known sequence. Such databases are fine-tuned to the size of the database used (Altschul et al., 1990, J. Mol. Biol. 215:403-410; Altschul et al., 1997, Nucleic Acids Res. 25:3389-3402), so that the same level of homology between a search sequence and a database sequence can be determined to be highly significant if the search sequence is compared with a smaller database, or insignificant and thus undetectable, if the search sequence is compared with a larger database.

In alternatives to standard homology searches, in projects oriented towards gene discovery, researchers usually have some *a priori* knowledge about the set of genes/proteins that might display important similarity to the unknown new gene. Therefore, selecting an *a priori* defined set of genes/proteins for comparison with new experimental sequences is a feasible and useful strategy. This strategy was successfully applied to search for homologs of disease genes in yeast and nematode genomes by Mushegian et al. (1997, Proc. Natl. Acad. Sci USA 94:5831-5836).

Two homologous genes taken from different species that originate from the nearest common ancestor by speciation are referred to as orthologs, while any two genes that originate from a common ancestor via a series of events involving intragenomic duplications are call paralogs. Tatusov et al. (1994, Proc. Nat.l, Acad. Sci USA 91:12091-12095) describe comparisons of proteins encoded by the genomes of different phylogenetic lineages and elucidation of consistent patterns of sequence similarities permitting the delineation of clusters of orthologous groups (COGs). Each COG consists of individual orthologous genes or orthologous groups of paralogs from different phylogenetic lineages. Since orthologs typically have the same function, the classification of known genes and proteins into clusters of orthologous groups permits the assignment of a function to a newly discovered gene or protein by merely classifying it into a COG. Although Tatusov describes a method for assigning a function to a newly discovered gene, he does not describe a method for predicting the existence of undiscovered genes. In addition, Yuan, et al. attempted simultaneous reconstruction of a species tree and identification of paralogous groups of sequences and detection of orthologs in sequence databases (Yuan et al., 1998, *Bioinformatics* 143:285-289).

Other groups have aimed at capturing interactions among molecules through the use of programs designed to compare structures and functions of proteins (Kazic 1994, In: Molecular Modeling: From Virtual Tools to Real Problems, Kumosinski, T. and Liebman, M.N. (Eds.), American Chemical Society, Washington, D.C. pp. 486-494; Kazic, 1994, In: New Data Challenges in Our Information Age Glaesar, P.S. and Millward, M.T.L. (Eds.). Proceedings of the Thirteenth International CODATA Secretariat, Paris pp. C133-C140; Goto et al., 1997, Pac. Symp. Biocomput. p. 175-186; Bono et al., 1998, Genome Res. 8:203-210; Selkov et al., 1996, Nucleic Acids Res. 24:26-28). These projects are significantly different from the inventive methods described herein because they do not describe methods for deducing the existence of as yet unknown genes based on comparisons of regulatory pathways and gene structure between one or more species. The present invention provides a method for increasing the sensitivity of analysis methods through the generation of specialized databases.

3. SUMMARY OF THE INVENTION

In accordance with the present invention there is provided methods for identification of novel genes comprising (i) generating one or more specialized databases containing information on gene/protein structure, function and/or regulatory interactions; and (ii) searching the specialized databases for homology or for a particular motif and thereby identifying a putative novel gene of interest. The invention may further comprise performing simulation and hypothesis testing to identify or confirm that the putative gene is a novel gene of interest.

The invention is based, in part, on the observation that functionally similar regulatory systems are generated during evolution by genetic duplication of ancestral genes. Thus, by comparing phylogenetic trees or regulatory networks and identifying genes and/or proteins absent in one system under comparison, the existence of as yet unidentified genes and/or proteins can be predicted. To make meaningful comparisons of phylogenetic trees it is necessary to distinguish between orthologs and paralogs. The present invention provides a method useful for discriminating between orthologs and paralogs and inferring the existence of as yet unidentified genes and/or proteins.

The present invention relates to natural language processing and extraction of relational information associated with genes and proteins that are found in genomics journal articles. Specifically, the natural language processing system of the invention is used to parse the articles published in biological journals focusing on structure and interactions among genes and proteins followed by computer representation of such interactions.

In accordance with the present invention, specialized databases are developed that contain information on gene/protein structure and interactions based on information derived from preexisting databases and/or research articles including information on interactions among genes and proteins, their domain/motif structure and their subcellular and tissue expression/distribution patterns.

The invention relates to a sequence analysis program which utilizes the specialized database for comparison of a single sequence, processing the output into a sequence alignment, computing phylogenetic trees, and analyzing these trees to

predict undiscovered genes. This program also includes a set of tools for generating motif/domain models from multiple sequence alignments of known genes and for using these models for extraction of structurally and/or functionally homologous sequences from databases which contain raw sequence data.

The invention further provides for a simulation and hypothesis testing program which relies on the specialized databases of gene/protein interactions for identifying potentially undiscovered members of multigene families through comparisons of regulatory networks for different species and testing hypotheses with regard to regulatory cascades. A comparison of homologous regulatory networks within the same organism and between different species of organisms will allow the identification of genes absent in one of the systems under comparison, thus providing a set of candidate genes. In this way, genes that contribute to the phenotype of a specific disease associated with a particular biological system under analysis may be identified, mapped and subjected to mutational analysis and functional studies.

4. BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a block diagram illustrating the three major programs of the method according to the present invention: (i) the generation of specialized databases based on information on gene/protein structure, function and regulatory interactions derived from research papers and databases; (ii) sequence analysis; and (iii) simulation and hypothesis testing;

Figure 2 is a block diagram of an information extraction system in accordance with a preferred embodiment of the present invention;

Figure 3 is a diagram illustrating the object representation of molecules and relations between them;

Figure 4 shows a set of keywords defining proteins involved in apoptosis pathways, these keywords having been utilized for generating a specialized sequence database Apoptosis3, this list having been compiled manually for testing the concept of specialized databases;

Figure 5 shows a "species tree," which is a graph depicting the correct order of speciation events leading to a set of present day species; a "gene tree," which

is a graph depicting a history of a few genes from the same species, where each species can be represented by multiple paralogous genes (because the set of known genes is incomplete for most genomes, and there are often multiple representations of the same gene family in the same genome, the gene tree can be drastically different from the corresponding species tree); and a "reconciled tree", which is the gene tree that would be obtained if gene deletions were completely forbidden and all genes were known for all species under analysis;

Figure 6 shows the original tree of ALDH sequences, indicating sequence clusters where bacterial, plant, fungal and nematode orthologous genes are present, but a human ortholog was not yet known;

Figure 7 shows the same phylogenetic tree as in Figure 6 with an additional human protein, referred to as antiquitin which was discovered by the method of the invention;

Figure 8 is a schematic diagram illustrating functional network-based gene discovery in accordance with the present invention;

Figure 9A presents diagrams depicting the regulatory relationships among hypothetical proteins (denoted with Arabic numerals) of hypothetical species A and B. Proteins in different species denoted with the same numeral are considered orthologous. The diagrams show that regulatory relationships between a pair of proteins can be of three different kinds;

Figure 9B, 9C, and 9D are diagrams representing Boolean operations OR, AND, and XOR, on arcs of the two oriented graphs of Figure 9A, the same operations being applicable to the set of vertices of the two oriented graphs;

Figure 10 is a diagram representing a hypothetical example of defining homologous protein networks in two different species using protein motifs, the diagram showing only two hypothetical proteins (1 and 2) for species A and three hypothetical proteins (1, 3, and 4) for species B. Protein 1 in both species has motifs α and β, protein 2 has motifs δ, ϵ, and ζ, and proteins 3 and 4 have motifs δ and ζ, and ϵ, respectively. The motif analysis can indicate that proteins 3 and 4 in species B may collectively perform the same function as protein 2 in species A;

Figure 11A and 11B are diagrams respectively representing hypothetical examples of evaluating the impact of a "knockout" of hypothetical gene A on the expression of a hypothetical gene B. The effect of knock-out of gene A calculated by multiplication along the shortest pathway connecting genes A and B is inhibition of gene B, the resulting effect being zero if the orientation of only one arc in the same pathway is reversed;

Figure 12 is a flow chart representing the scheme of gene discovery analysis involving motif/domain analysis in accordance with the present invention; and

Figure 13 Identification of genes in *C. elegans* containing either POZ or kelch domains. The protein excession numbers are indicated adjacent to the different protein domains. The protein corresponding to accession number gi/1132541 contains a POZ domain, death domain, kinase domain and heat repeat.

Figure 14A. Two human sequences with the closest homology to the *C. elegans* sequence gi/1132541.

Figure 14B. Computed gene tree indicating that the identified human gene represents an ortholog of the *C. elegans* gene gi/1132541.

Figure 14C. Nucleotide sequence of the death domain gene.

Figure 14D. Deduced amino acid sequence of the death domain protein.

Figure 15. Identification of candidate gene implicated in the etiology of Chronic Lymphocytic Leukemia (CLL). Sequence homology between a CLL region open reading frame and mouse Rpt1 (sp/P15533/RPT1) is presented.

Figure 16A-B. Model of regulatory functions of Rpt1. Figure 16A indicates that in mouse T lymphocytes Rpt1 serves as a repressor of the gene for interleukin 2 receptor (IL-2R). Figure 16B demonstrates that when Rpt1 is knocked out, the regulatory effect is manifested as a block of the apoptotic pathway for T-lymphocytes resulting in accumulation of T-lymphocytes in blood.

Figure 17A. Two EST sequences identified by searching a protein dbEST using the mouse Mad3 protein as a query.

Figure 17B. Nucleotide sequence of the human Mad3 gene.

Figure 17C. Complete sequence of the human Mad3 protein. A search was conducted to identify overlapping sequences. The complete sequence of the gene was assembled and the amino acid sequence deduced. The translated human Mad3 sequence consists of 206 amino acid residues 81% of which are identical to the mouse Mad3 protein.

Figure 17D. Multiple alignment of the human Mad3 amino acid sequence with known Mad proteins.

Figure 18A. Phylogenetic tree indicating relationship between three known mouse Mad genes and their two human homologs.

Figure 18B. Phylogenetic tree including new human Mad3 sequence. The phylogenetic tree indicates that the new human gene belongs to the family of Mad proteins and is an ortholog of mouse Mad3.

5. DETAILED DESCRIPTION OF THE INVENTION

The present invention provides methods for identification of novel genes comprising: (i) generating specialized databases containing information on gene/protein structure, function and regulatory interactions and, (ii) sequence analysis which includes homology searches and motif analysis thereby identifying a putative novel gene of interest. The invention may further comprise performing simulation and hypothesis testing to identify or confirm that the putative gene is a novel gene of interest.

The specialized databases are constructed utilizing information concerning gene/protein structure or function derived from unpublished data, research articles and/or existing databases. The specialized databases can be used to identify novel genes by: (i) searching for motif/domain combinations characteristic for a putative gene of interest; (ii) phylogenetic tree analysis of homologous genes for predicting the existence of yet undiscovered genes; (iii) comparing members of interactive gene/protein networks from different species for predicting the existence of yet undiscovered genes; and (iv) testing a hypothesis with regard to known interactions of homologs from other species in regulatory pathways.

5.1. THE NATURAL LANGUAGE PROCESSING

The present invention relates to a natural language processing system that is designed to parse the electronic versions of articles published in journals that report on structural interactions among genes and proteins. The system provides a method for extracting information on interactions among genes and proteins, their domain/motif structure, and/or their sub-cellular and tissue expression/distribution patterns, followed by computer representation of such information.

The general natural language-processing system of the invention is schematically depicted in Figure 2. The collection phase automatically collects articles from appropriate literature, and selects articles that contain relevant information using Keyword search techniques. In the next phase, the preprocessor standardizes the selected articles so that they consist of tagged ASCII text where the tags delineate critical components of the article. The next phase, termed the extraction phase, retrieves and classifies biological entities, *i.e.*, as names of proteins, genes and small molecules. In addition, the relationship extraction phase recovers structural relationships between the entities. This phase is followed by a phase which performs an analysis of the sequence of events.

The final phase of the system processes the output extracted from an article to remove redundancies, inconsistencies and to incorporate implicit information before adding the extracted knowledge consisting of biological entities, their attributes, conditional constraints, and relationships between them, for subsequent use in analysis and hypothesis testing. The information extraction system as depicted in Figure 2, referred to herein as "GENIE," is designed for use as a general processor within the domain of genomics literature although the system may also be used in other specialized domains. GENIE is an adaptation of MedLEE developed for the medical domain. GENIE uses the same source code as MedLEE but the Lexicons and grammar were adapted for genomics literature.

The information extraction system of the present invention is described below, by way of example, with reference to the genomics domain uses of GENIE. It is written in Quintus Prolog and uses the Unix or Windows operating systems, as described in detail below.

A natural-language phrase included in text document is understood as a delimited string comprising natural-language terms or words. The string is computer readable as obtained, *e.g.*, from a pre-existing database, a keyboard input, optical scanning of typed or handwritten text, or processed voice input. The delimiter may be a period, a semicolon, an end-of-message signal, a new-paragraph signal, or any other suitable symbol recognizable for this purpose. Within the phrase, the terms may be separated by another type of delimiter such as a blank or another suitable symbol.

As a result of phrase parsing, terms in a natural-language phrase are classified, (*e.g.*, as referring to a gene, a protein, or their interactions) and the relationships between the interactions are established and represented in a standard form. For example, in the sentence "Rap inhibited fyn", the structured form would be:

[action,inactivate,[protein,rap],[protein,fyn]].

In such an example, the interaction is "inactivate", the agent is "Rap" and the target is "fyn." More complex sentences consisting of nested relationships, such as "The activation of BAD was suppressed by the phosphorylation of JNK" can also be parsed and represented appropriately. The structured output form for this sentence would be: [action,inactivate,[action,phosphorylate,x,[protein,jnk],[action,activate,x,[protein,bad]
]

In the first example, the primary interaction is "inactivate"; in the second example, an interaction "phosphorylate" is the agent where the protein "jnk" is its target (the agent of "phosyphorylate" in not specified and thus is represented as "x"). In this example, the target of "inactivate" is also an interaction "activate" where the target is the protein "bad" and the agent is unknown.

While parsing is based on both syntactic and semantic grammatical patterns, the substances in a domain are normally only semantic categories such as "protein", "gene", and "small molecule." There are no corresponding syntactic categories needed for these substances because they are normally all nouns. However, each action can be categorized both semantically and syntactically. An action, which is a semantic category, can generally occur syntactically as a verb "inactivate" or as a noun "inactivation." Therefore there are two sets of lexical entries for the actions:

syntactic and semantic. The syntactic lexicon for actions specifies the main syntactic category such as "v" for verb, "ving" for progressive form of verb, and "activation" for noun. The semantic entries for actions not only categorize the actions, but also specify features for each action. For example, one feature provides the number of arguments that are expected for the action, *i.e.*, some actions are associated with two arguments because they have an agent and a target as "inactivate", and others just have an agent "mutate." The lexicon of substances and structures appears as Appendix A; the syntactic lexicon for actions appears as Appendix B; and the semantic lexicon of actions appears as Appendix C.

A second feature specifies whether or not the arguments should be reversed when obtaining the target form. For example the arguments of "attributable to" should be reversed, *i.e.*, in "the phosphorylation of jnk is attributable to the activation of bad", the underlying action is "cause" (from "attributable to"), the agent is the "activation of bad" and the target is "the phoshorylation of jnk"), whereas the arguments of "activates" is not(i.e. in "jnk activates bad" , the agent is "jnk" and the target is "bad").

Figure 2 shows a preprocessor module of GENIE by which natural-language input text is received. The preprocessor thus performs lexical lookup to identify and categorize multi-word and single word phases within each sentence. The output of this component consists of a list of word elements where each element is associated with a word or multi-word phrase in the report. For example, assuming that the sentence "bad functions as a negative regulator of the activation of jnk" is at the beginning of the report, it would be represented as a list of elements where each element is a word or phrase. For example, element 1 is associated with "bad", element 2 with the multi-word phrase "functions as a negative regulator of", element 8 with "the", and element 9 with "activation". The remainder of the list of word positions would be associated with the remaining words in the report. Some of the phrases may not need lexical lookup because they already have been tagged by a previous component. Such a tagging system is described below in Section 5.2.

The second component of the GENIE system is the parser. It utilizes the grammar and categories assigned to the phrases of a sentence to recognize well-

formed syntactic and semantic patterns in the sentence and to generate structured output forms. The parser proceeds by starting at the beginning of the sentence element list and following the grammar rules. When a semantic or syntactic category is reached in the grammar, the lexical item corresponding to the next available unmatched element is obtained and its corresponding lexical definition is checked to see whether or not it matches the grammar category. If it does match, the word or phrase is removed from the unmatched sentence list, and the parsing proceeds. If a match is not obtained, an alternative grammar rule is tried. If no analysis can be obtained, an error recovery procedure is followed so that a partial analysis is attempted. The actual grammar used for GENIE appears as Appendix D.

The parser module of GENIE uses the lexicon, and a grammar module to generate target forms. Thus, in addition to parsing of complete phrases, subphrase parsing can be used to an advantage where highest accuracy is not required. In case a phrase cannot be parsed in its entirety, one or several attempts can be made to parse a portion of the phrase for obtaining useful information in spite of a possible loss of information.

Conveniently, each module is software-implemented and stored in random-access memory of a suitable computer, *e.g.*, a work-station computer. The software can be in the form of executable object code, obtained, *e.g.*, by compiling from source code. Source code interpretation is not precluded. Source code can be in the form of sequence-controlled instructions as in Fortran, Pascal or "C", for example. Alternatively, a rule-based system can be used such a Prolog, where suitable sequencing is chosen by the system at run-time.

An illustrative portion of the GENIE system is shown in the Appendix D in the form of a Prolog source listing with comments. The following is further to the comments.

Process_sents with *get_inputsents, process_sects* and *outputresults* reads in an input stream, processes sections of the input stream according to parameter settings, and produces output according to the settings, respectively. Among parameters supplied to *Process_sents* are the following: Mode (specifying the parsing

mode) and Protocol (html or plain). *Process_sents* is called by another predicate, after user-specified parameters have been processed.

The parsing modes are selected by GENIE so as to parse a sentence or phrase structure using a grammar that includes one or more patterns of semantic and syntactic categories that are well-formed. For example, for the phrase "bad inactivates jnk", a legitimate pattern can be substance1 action substance2, wherein substance1 = protein bad, action = "inactivates" and substance2 = "jnk." However, if parsing fails, various error recovery modes are utilized in order to achieve robustness. The error recovery techniques use methods such as segmenting the sentence, processing large chunks of the sentence, and processing local phrases. Each recovery technique is likely to increase sensitivity but decrease specificity and precision. Sensitivity is the performance measure equal to the true positive rate of the natural language processing, *i.e.*, the ratio of information extracted by the natural language processing system that should have been extracted. Specificity is the performance measure equal to the true negative information rate of the system, *i.e.*, the ratio of information not extracted by the NLP system that should not have been extracted. Precision is the reliability of the system, *i.e.*, the ratio of information extracted correctly compared to all the information that was extracted. In processing a report, the most specific mode is attempted first, and successive less specific modes are used only if needed.

In accordance with the preferred embodiments of the present invention, the parser of Figure 2 includes five parsing modes, Modes 1 through 5, for parsing sentences or phrases. Nominally, the parser is configured to first select Mode 1. If Mode 1 is not possible, the program continues with Mode 2 and so forth until parsing is complete. With Mode 1, the initial segment is the entire sentence and all words in the segment must be defined. This mode requires a well-formed pattern for the complete segment.

Mode 2 requires that the sentence or phrase be segmented at certain types of words or phrases, *e.g.*, " is attributable to." Here, an attempt is made to recognize each segment independently, *i.e.*, a first segment ending with the word "is" and a second segment beginning with the word after "to." The segmenting process is

repeated until an analysis of each segment is obtained or until segmenting is no longer possible.

Mode 3 requires a well-formed pattern for the "largest" prefix of the segment, *i.e.*, usually at the beginning of the segment. This occurs when a sentence contains a pattern at the end which is not in the grammar but a beginning portion that is included. For example, in "bad inactivates jnk at this time", the beginning of the sentence "bad inactivates jnk" will be parsed and the remainder will be skipped.

Mode 4 requires that undefined words be skipped and an analysis be attempted in accordance with Mode 1. Mode 4 is useful where there are typographical errors and unknown words. For example, in the phrase "abc bad inactivates jnk", the word *abc* is unknown to the system and will be ignored but the remainder of the phrase will be parsed.

Mode 5 first requires that the first word or phrase in the segment associated with an action be found. Next, an attempt is made to recognize the phrase starting with the leftmost recognizable argument. For example, in "during bad inactivates jnk on the fifth day," the phrase "bad inactivates jnk" will be parsed and the remaining words will not be. If no analysis is found, recognition is retried at the next possible argument to the right. This process continues until an analysis is found.

Process_sects with *get_section* and *parse_sentences* gets each section and generates intermediate output for the sentences in each section.

Write produces the output as a list consisting of relations and interactions

Setargs sets arguments or parameter values based on user input or by default.

The structured output generated by the GENIE program uses a frame-based representation. Each frame specifies the informational type, the value, and arguments or modifier slots which are also frames. Consider the text data input "bad inactivates the phosphorylation of jnk." A corresponding output, as shown below, is a frame denoting an action, which has the value inactivate; in addition, there are two arguments. The first argument is a protein bad and the second argument is an action with the value phosphorylate, which has two arguments. The first argument is x

signifying that the agent has not been specified; the second argument is a protein with the value jnk. The second argument is the target:

[action,inactive,[protein,bad],[action,phosphorylate,x,[protein,jnk

In summary, a computer system has been disclosed that generates structured information concerning protein and gene interactions and relationships.

5.2. USE OF BLAST FOR FINDING GENE AND PROTEIN NAMES IN JOURNAL ARTICLES

In a specific embodiment of the invention, an exhaustive list of gene and protein names, extracted from GeneBank, is translated into a different alphabet system by substituting each character in the name with a predetermined unique nucleotide combination. The encoded names are then imported into the BLAST database using the FASTA format. The scientific journals are translated, using the same nucleotide combinations, into a continuous string of nucleotides. A query is then used to match the translated journals against the nucleotide representation of gene and protein names in the BLAST database. Significant alignments associated with gene and protein names are listed in the BLAST output file, which is subsequently processed using Perl-scripts. The final result consists of the original journal article with XML tags surrounding the gene and protein names.

To adapt the problem to BLAST's statistical foundation, different measures were undertaken to limit the output to the most relevant gene and protein names. In addition, in order to fine-tune the matching process, different BLAST parameters were adjusted, such as the *word size* (which sets the size of the high scoring words, thus influencing the sensitivity of finding HSPs) and *mismatch penalty* (exact vs approximate matching).

In a specific embodiment of the invention, gene and protein names are extracted from GeneBank's gene symbol index file. The following is an excerpt of the file after discarding entries that are either composed of only numbers or of less than two alphabetic letters:

gfap gamma

hox a10

hox a1

wac 3'-end

pit-1/ghf-1 variant

[...]

This list of gene and protein names is translated into a different alphabet system by substituting each character in the name with a predetermined unique nucleotide combination. The conversion chart is listed in Appendix E. The encoded names are then imported into the BLAST database using the FASTA format. For example, the first entry in the list above is "gfap gamma." After translation using the conversion chart, the same name appears as follows:

AGCAACTAAACACCCATCCAAGCAAACACACACACAAAC

Thus, the complete FASTA entry looks like this:

>gi|1 species,gp,gfap gamma

AAGCAACTAAACACCCATCCAAGCAAACACACACACAAAC

In FASTA, the definition line (marked with '>') contains information about the database entry. This line can contain any kind of information. The information important for this particular example is the third entry in the definition line, 'gp', that specifies that the name can represent a gene *or* a protein. If the name is unambigous, then the definition line states that the name is only associated with a gene ('g') or protein ('p'). The fourth entry in the definition line is the name of the protein or gene, "gfap gamma" in this case.

The second line in the FASTA format normally contains the actual sequence of the protein/gene. In the example presented, the second line contains the translated protein or gene name.

All gene and protein names are translated into the nucleotide representation and converted into the FASTA format. Then, the database containing these FASTA entries are specially compiled for use in BLAST queries using a program that is included in the BLAST package called "formatdb".

Thus, the scientific journals are translated, using the same nucleotide combinations, into a continuous string of nucleotides. For example, the sentence "In

the absence of costimulation, T cells activated through their antigen ..." is translated into

"AAGTACAGATCCACGGAAGGAACGATCCAAACAAAGACGCAACGACAG
AAATAACGATCCACATAACTATCCAAATACATACGCACGGAAGTACACAC
GTAATTAAACACGGAAGTACATACAGATCCATCCACGGATCCAAATAACG
AATTAATTACGCATCCAAACAAATACGGAAGTACTCAAACACGGAACGAA
CCATCCACGGAAGGACCTACATACGTAAGCAAGGATCCACGGAAGGAAC
GAAGTACCTATCCAAACACAGACGGAAGTAAGCAACGACAGATCC "

A query is then used to match the translated journals against the nucleotide representation of gene and protein names in the BLAST database. The query is executed using the blastall program that is included in the BLAST package. The query line looks like:

blastall -p blastn -d FASTA.dat -i query.txt

The flag 'p' denotes the sub-program (blastn is a sub-program of blastall that performs nucleotide matches), 'd' denotes the file that contains the FASTA entries and 'i' denotes the translated query text.

Significant alignments associated with gene and protein names are listed in the BLAST output file. This is an excerpt from a BLAST output file:

gi|63624 species,gp,ner
Length = 12
Score = 24.4 bits (12), Expect = 3e-05
Identities = 12/12 (100%)
Strand = Plus / Plus
Query: 729 acagaacgacct 740
Sbjct: 1 acagaacgacct 12

The first line denotes the database entry. The second line denotes the database sequence length, followed by the alignment score and the E-value. The next line indicates paired matches, mismatches and gapped alignment (the latter two are not shown in this example). The lines 'Query' and 'Sbjct' show the actual alignment between the query and database sequence. This output file is subsequently processed

using a Perl-script (see Appendix F). The script shown in Appendix G scans the output file, which is sometimes several megabytes long, for any segments that start at position 1 of the database sequence (thus disregarding any segments that are only part of the sequence). In addition, the script allows for 10% mismatches between the aligned sequences for long sequences (as shown in the script of Appendix E), or 0% mismatches for short sequences. After scanning the output file, an intermediary file that lists the candidate sequences is created:

tran|365|381|gp|18493
tran|1|17|gp|18493
peci|549|565|gp|58106
il-2|621|637|gp|82396
il-2|325|341|gp|82396
gati|193|209|gp|92088
prod|641|657|gp|52292
rap1|105|121|gp|49898
spec|545|561|gp|33183
crip|385|401|gp|118905
crip|21|37|gp|118905
as|161|177|gp|133961
her|65|77|gp|88411

The intermediary file lists the name of the sequence, followed by the starting and end point in the query sequence (corresponds to where the two sequences matched), the semantic class of the name (protein, gene or protein/gene). The last number is not considered.

The intermediary file is then scanned by another Perl program (Appendix G). This program compares the starting end points with the actual text, making sure that the matched name is an 'autonomous' entity in the query text. For example, while "per" in " per gene" should be recognized as a gene name, "per" in "personal" should not be recognized as a gene name. The program recognizes other characters than the space character delimiting an 'autonomous' gene or protein name.

In addition, the script looks for plurals of words. For example, " interleukins" should be recognized as a protein name, although only the singular form, "interleukin", is in the database.

The final result consists of the original journal article with XML tags surrounding the gene and protein names. This is done using the same script as in Appendix G:

blocked <phr sem="gp">T cell antigen receptor</phr> (TCR)- and <phr sem="gp">CD28</phr>-mediated <phr sem="gp">IL-2</phr> gene transcription. Therefore, <phr sem="gp">Rap1</phr> functions as a negative regulator of...

To adapt the problem to BLAST's statistical foundation, different measures were undertaken to limit the output to the most relevant gene and protein names.

BLAST is sensitive to the search space the program works in. Thus, given a long query sequence and a large sequence database, matches have a lower statistical significance because the chances are higher that the matches could have occurred by chance alone. In addition, matches with few letters have a lower statistical significance than matches with many letters. In order to find all true matches with any significance level, some measures were undertaken to address this problem. For example, (i) the query sequence was divided into 10 equal length parts, *i.e.*, the journal article was divided into 10 parts and 10 different queries are run on each part separately; (ii) the sequence database (with the gene and protein names) is separated into 5 databases, each containing protein/gene names of different length; (iii) gene and protein names with less than 3 letters in the database were 'expanded', *i.e.*, spaces were added at the beginning and the end of the name. Doing so, the statistical significance of a match containing a short name was higher. A space does not only include an empty character. For example, a gene name "k4" could occur in a journal article as "kinin 4 (k4)". It was therefore important to define several characters as substitutes for a space character. The alphabet in Appendix E defines the nucleotide combination ATCC as such a substitute.

Working with nucleotides implies that errors involving reading frames must be addressed. For example, working with a code of four letters, the nucleotide combination ATCTGTCACG could mean ATCT/GTCA or TCTG/TCAC or CTGT/CACG . Since the text is translated into a nucleotide combination, only one of these possibilities is correct. But BLAST can not distinguish between these solutions, *i.e.*, BLAST would potentially match a database sequence to a wrong reading frame in the query sequence, producing many nonsense results that could compromise the significance of true results.

The solution to this problem is a comma-free code. A comma free code knows only one correct reading frame. BLAST therefore does not produce any nonsense results. A comma-free code consists of only one permutation of a nucleotide combination. For example, given the nucleotide combination ATCC and its permutations CATC, CCAT and TCCA, only ONE of these permutations would be included in a comma-free code. The code in Appendix E does represent a comma free code. Comma-free codes were discussed in the early days of DNA research (Crick et al., Proc. Natl. Acad. Sci. 43:416-421).

In order to fine-tune the matching process, different BLAST parameters must be adjusted, for example: *word size* (which sets the size of the high scoring words, thus influencing the sensitivity of finding HSPs);*mismatch penalty* (exact vs approximate matching); *numbers of alignments to show* (true matches of low significance can sometimes be at the very end of the BLAST output, therefore many alignments have to be shown); and *expectation value* (which sets the significance value for matches in the output file).

5.3. GENERATION OF SPECIALIZED DATABASES

In accordance with the present invention, specialized databases may be developed that contain information derived from unpublished data, publications such as research articles, theses, posters, abstracts, etc. and/or databases concerning interactions among genes and proteins, their domain/motif structure, and their biological functions.

For example, but not by way of limitation, a specialized database may be prepared as follows. Protein and gene sequences may be provided, for example, by the Java program PsiRetrieve which allows for quick retrieval of protein or nucleotide sequences from binary BLAST databases by sequence accession number, keyword or groups of keywords, or species name. In addition, using the program PsiRetriever, sequences encoding the proteins of interest may be retrieved from the non-redundant (NCBI) database of protein sequences and stored as a FASTA file. The FASTA file is then converted into a binary blast database using the program FORMATDB from the BLAST suit of programs.

Known motifs/domains for proteins may also be collected using the flat file versions of major protein databases, such as SwissProt (http://expasy.hcage.ch/sprot) and the non-redundant database of NCBI (http://www3.ncbi.nlm.nih.gov). The databases can be downloaded and searched for the keywords "motif" and "domain" in the feature tables of proteins. In addition, existing databases of motifs and domains, such as BLOCKS (http://dupsas.Weizmann.ac.il/bcd/bcdparent//databanksblocks/hfml) and pfam(http://www.sanger.ac.uk//software/pfam; http://pfm.wustl.edu), can be downloaded (Henikoff et al., 1991, NAR 19:6565-6572). Still further, it is understood that any publically available database containing gene/protein sequences may be utilized to generate the specialized databases for use in the practice of the present invention.

Homologous sequences may be aligned using, for example, the CLUSTALW program (Higgins, et al. 1996 Methods in Enzymology 266: 383-402). A protein's sequence corresponding to each domain/motif can be identified, saved and used for building a Hidden Markov Model (HMM) of the domain/motif using a HMMER and HMMER2 packages (see, Durbin, R. et al. 1998 in Biological Sequence Analysis: Probablistic Models of Proteins and Nucleic Acids). HMMER and HMMER2 packages are useful for (i) building HMMs from sets of aligned protein or nucleotide sequences, and (ii) comparing the HMMs with sequence databases aimed at identifying significant similarities of HMMs with database sequences. Both nucleotide and protein databases can be used for this purpose. Alternatives to the

Hidden Markov Model method for building domain/motif models include neural network motif analysis (Wu, C.H. et al., 1996, Comput Appl Biosci 12, 109-18; Hirst, J.D., 1991, Protein Eng 4:615-23) and positional weight matrix analysis (Claverie, J.M., 1994, Comput Chem 18:287-94; Venezia, D., 1993, Comput Appl Biosci 9:65-9; Bucher, P. 1996, Comput Chem, 20:3-23; Tatusov, R.L., 1994, Proc Natl Acad Sci USA 91:12091-5).

Once a comprehensive collection of motifs/domains is created, each particular protein may be compared against a complete database of HMMs to identify known motifs and domains.

The Hidden Markov Model (HMM) is built using the following steps:

A1. Start with a motif/domain name and a single amino acid sequence representing a domain or motif.

A2. Do PSI-BLAST (BLASTPGP) search with the motif/domain sequence against a protein non-redundant database.

A3. Retrieve the sequences identified in the database search from the protein sequence database. Exclude low-complexity sequences, short or incomplete sequences and sequences with similarity score above a selected threshold of PPD value <0.001

A4. Align the set of sequences with CLUSTALW (or other multiple sequence alignment program).

A5. Use the set of aligned sequences for building HMM with the programs provided with HMMER and HMMER2 packages (see Hughey and Krogh 1996, J. Mol. Biol. 235:1501-1531).

A6. Do a new database search comparing new HMM with the non-redundant protein database.

A7. Continue steps A3-A6 until the convergence of the Markov model *i.e.*, until no new sequences are identified, or the maximum allowed number of iterations as defined by the user is reached. (Hugh R. and Krogh A., 1996, Comput. Appl. Biosci. 12: 95-107).

In addition, in yet another embodiment of the invention, a specialized database may be designed to contain a semantic model of proteins and of the possible

interactions between them. Such databases are particularly useful for computation and analysis of regulatory networks between proteins. The semantic model is designed for representing substances, such as proteins and actions between them, and is based on widely accepted principles of object-oriented programming languages such as Java. Figure 3 is a diagram illustrating the object representation of molecules and relations between them. As indicated in Figure 3 there are six major classes, corresponding to the top-level classification of objects and actions: (*i*) a substance; (*ii*) a state of a substance; (*iii*) a similarity between substances; (*iv*) an action between substances; (*v*) a result of the action; and (*vi*) a mechanism that enables an action.

Figure 3 presents the class design graphically, listing the variables that represent the properties of each class or class object in the implementation. Classes can be made nested via the mechanism of "inheritance", *i.e.*, classes are defined starting with the most general ones and moving towards more specific classes. Definition of more specific classes is simplified because the properties of the general classes are "inherited" by the specific classes and need not be redefined each time (see, Flanagan 1997, Java in a Nutshell, Second Edition. O'Reilley & Associates, Inc. Sebastopol, CA).

As shown in Figure 3, the two key object types in this scheme are substances (nodes of the graph representing regulatory networks) and actions (oriented edges connecting pairs of nodes), while result and mechanism objects are auxiliary to object action. Each substance object is characterized with a state. In this scheme, action is the most complicated object; each action object is characterized by a specific pair of substances participating in the action, one of which can be active and is referred to as Subject Substance and the second of which can serve as a substrate for the former and is referred to as Object Substance. Furthermore, for each action the initial and final states corresponding to interacting substances are defined. The property Time Required of each Action Object allows the setting of different durations for different actions (time is measured in relative units; see René Thomas and Richard D'Ari, 1990, "Biological Feedback," CRC Press Boca Raton, Ann Arbor, Boston).

Once developed, the specialized databases can be used to identify novel genes based on computation and analysis of phylogenetic trees for multigene families and analysis of homologous regulatory networks.

In a specific embodiment of the invention, a specialized database was generated using a set of keywords defining proteins involved in apoptosis (see, Figure 4). The specialized sequence database was referred to as Apoptosis 3. As a first step in generating the specialized database, a comprehensive set of articles describing the system of apoptosis or programed cell death was compiled. The articles were analyzed and information on regulatory pathways characterizing apoptosis from a variety of different organisms was extracted. Such pathways included those involved in MHC-T cell receptor interactions, inflammatory cytokine signal transduction, induction by light, γ-radiation, hyperosmolarity or heat shock, pathways involving immunoregulatory receptors or receptors having cytoplasmic domains, integrin-related pathways and perforin/granzymeβ related pathways. The collected information was stored using Powerpoint (Microsoft) as a collection of graph/plots depicting the regulatory pathway. In addition, a list of proteins relevant to regulation of apoptosis was compiled.

Using the program Psi Retriever, sequences encoding the proteins relevant to regulation of apoptosis were retrieved from the non-redundant (NCBI) database of protein sequences and stored as a FASTA file. The FASTA file was then converted to a binary blast database using the program FORMATDB from the BLAST suit of programs. The BLAST suit of programs provides a set of programs for very fast comparisons of a single sequence to a large database. Both the database and the search or query sequence can be any combination of nucleotide and/or amino acid sequences.

In a working example described herein, the Apoptosis 3 database was used to compare genomic and cDNA sequences derived from the 13q region of human chromosome 13. This region of the chromosome is associated with Chronic Lymphocytic Leukemia (CLL). Using this method of analysis a human gene with significant homology to the mouse Rpt1 gene was identified. When the activity of Rpt1 is knocked out in mice, the regulatory effect is manifested as a block in T-

lymphocyte apoptosis. This result indicates that the identified human Rpt1 homology may represent the gene in which genetic defects lead to CLL.

The amino acid sequence of the human Rpt1 gene is presented in Figure 15. The present invention relates to nucleic acid molecules encoding the human Rpt1 protein shown in Figure 15. The invention also relates to nucleic acid molecules capable of hybridizing to a nucleic acid molecule encoding the human Rpt1 protein presented in Figure 15 under conditions of high stringency. By way of example and not limitation, procedures using such conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 hours to overnight at 65°C in buffer composed of 6x SSC, 50 mM Tris-HCl (pH7.5), ImM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA and 500 mg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65°C in prehybridization mixture containing 100mg/ml denatured salmon sperm DNA and 5-20 x 10^6 CpM of ^{32}P-labeled probe. Washing of filters is done at 37°C for 1 h in a solution containing 2x SSC, 0.01% PVP, 0.01% Ficoll and 0.01% BSA. This is followed by a wash in 0.1 x SSC at 50°C for 45 minutes before autoradiography. Other conditions of high stringency which may be used are well known in the art.

5.4. GENE DISCOVERY THROUGH PHYLOGENETIC ANALYSIS OF GENE FAMILIES

The present invention provides a method for identifying novel genes comprising the following steps: (i) comparing a single sequence with a database; (ii) processing the output into a sequence alignment; (iii) computing gene trees; and (iv) analyzing the trees to predict the existence of undiscovered genes.

Figure 5 shows a "species tree," a "gene tree" and a "reconciled tree". A "species tree", as defined herein, is a graph depicting the correct order of speciation events leading to a set of present day species as defined by taxonomy. A "gene tree" is a graphical representation of the evolution of a gene from a single ancestral sequence in a common progenitor to a set of present-day sequences in different species. Where gene duplication has occurred, a branch is bifurcated. The branch lengths of a gene tree are most frequently measured either in terms of the number of

amino acid or nucleotide replacements per site or in terms of millions of years (absolute geological time). In the former case, the average replacement rate in the majority of the published trees varies among tree branches, and the root-to-tip distances are different for different present day sequences. In the latter case, all root-to-tip distances are equal and the height of each interior node of the tree corresponds to the absolute geological time passed since the gene duplication corresponding to the interior node took place.

If a gene is unique, *i.e.*, represented with a single copy per genome rather than being a member of a family of similar genes, the correct gene tree depicting the origin of this gene in a few different species is identical to the species tree. In many instances, a single ancestral gene has been duplicated repeatedly during evolution to form a multigene family. A gene tree is constructed from a gene as it occurs in several species and reflects both speciation events and gene duplications within the same genome. Two homologous genes taken from different species that originated from the nearest common ancestor by speciation are referred to as orthologs, while any two genes that originated from the common ancestor via a series of events involving intragenomic duplications, or conversions, are called paralogs. The terms "ortholog" and "paralog" are applied to both nucleic acid and proteins herein.

If gene deletions are forbidden and all genes for all species represented in the tree are known, the gene tree can be reconfigured to recapitulate the species tree, such that each subtree contains only orthologous genes. This tree is referred to as a reconciled tree and is shown in Figure 5. Imperfect gene trees which contain incorrect or partial species subtrees can be used to build reconciled trees that indicate events of speciation, gene loss, and gene duplication.

Orthologs from different species in gene trees are usually clustered together, so that if all the existing homologous genes from different species were known, the same relationship of species would be recapitulated in each cluster of orthologous genes. Since in reality a considerable number of genes are not yet identified, the real gene trees contain incomplete clusters of orthologs that can be used for identification of the missing genes.

By applying phylogenetic analysis, *i.e.*, reconstruction of gene trees of gene/protein sequences, one can predict the existence of undiscovered genes in humans and other species in addition to identifying the function of a gene. Such a technique is a significantly more powerful tool for identification of new genes than mere sequence comparisons.

Methods of computing gene trees from a set of aligned sequences include the : (i) heuristic method based on an optimization principle which is not directly motivated by a probability model (Fitch, 1974 J. Mol. Evol. 3:263-268)), (ii) the maximum likelihood method (Goldman, 1990, Syst. Zool. 30:345-361; Yang et al., 1995, Syst. Biol. 44:384-399; Felsenstein, J., 1996, Methods Enzymol. 266-418-427); and (iii) the distance matrix tree making method (Saito, N. and Nei, M., 1987, Mol. Biol. Evol. 4:406-425). Since the data analyses of orthologs and paralogs often involve very distantly related sequences, the maximum likelihood method is preferably used for small data sets and the distance-matrix method in other instances.

To construct a reconciled tree according to the invention, the first step comprises a search for homologs in a publicly or privately available database such as, for example, GenBank, Incyte, binary BLAST databases, Swiss Prot and NCBI databases. Following the identification of homologous sequences a global alignment is performed using, for example, the CLUSTALW program. From the sequence alignment a gene tree is constructed using, for example, the computer program CLUSTLAW which utilizes the neighbor-joining method of Saito and Nei (1997, Mol. Biol. Evol. 4:406-425). Construction of a species tree is then retrieved from, for example, the following web site:
http://www.3.NCBI.NLM.NIH.GOV//taxomy.tax.html.

The species tree and gene tree are given as input into the algorithm described below, which integrates both trees into a reconciled tree. Agreement between the gene tree and the corresponding species tree for any given set of sequences indicates the identification of orthologs. In contrast, disagreement between the species and gene tree suggest a gene duplication that resulted in the formation of a paralog. Thus, through generation of a reconciled tree one can identify orthologs present in one species but missing in another. These can be deduced by forming

subtrees of orthologs in a gene tree, and then comparing the subtree in the gene tree with a species tree. A missing gene appears as a branch present in the species tree but absent in the gene tree. The algorithm for defining an orthologous gene subtree and predicting the undiscovered, or lost in evolution, genes is as follows:

Let T_g be the most likely gene tree identified with one of consistent tree-making methods from a set of properly aligned homologous genes {1, 2, ..., s}, such that one or more homologous genes from every species corresponds to pending vertices of T_g. Each gene is labeled with the species it comes from (1,...,s) adding subscripts to distinguish homologous genes from the same species whenever it is necessary. Let T_g be the true species tree (tree correctly reflecting speciation events which we assume to be known) for species {1, 2, ..., s}. Due to the biological meaning of T_s each species in this tree is represented only once. It is assumed that both T_s and T_g are binary, although it is straightforward to extend the algorithm described here to the case of multifurcated trees.

<u>Algorithm</u>

A1. For each pair of interior nodes from trees T_g and T_s, compute similarity $\sigma(S_{gi},S_{sj})$.

A2. Find the maximum $\sigma(S_{gi},S_{sj})$.

A3. Save S_{gi} as a new subtree of orthologs, save $\{S_{gi}\}$ - $\{S_{sj}\}$ as a set of species that are likely to have gene of this kind (or lost it in evolution).

A4. Eliminate S_{gi} from T_g; $T_g := T_g \backslash S_{gi}$.

A5. Continue A2 - A4 until T_g is non-empty.

The following definitions apply:

Let S_{gi} be an *i*th subtree of T_g (corresponding to the *i*th interior node), correspondingly, let S_{sj} be *j*th subtree of tree T_s.

Let $\{S_{gi}\}$ stand for an unordered set of species represented in S_{gi} such that each species is represented exactly once, and let $|\{S_{gi}\}|$ and $\{|S_{gi}|\}$ be the number of entries in $\{S_{gi}\}$ and the number of pending vertices in S_{gi}, respectively. Define by $S_{sj}(S_{gi})$ the unique subtree of S_{sj} that has leaves labeled exclusively with species from $|\{S_{gi}\}|$, so that each element of $|\{S_{gi}\}|$ is used i.e., that is, the unique subtree obtained by eliminating from S_{sj} all species that are not present in $|\{S_{gi}\}|$.

Then define similarity measure, σ, between S_{gi} and S_{sj} in the following way:

$\sigma(S_{gi},S_{sj}) = 0$ if $|S_{gi}| \neq |\{S_{gi}\}|$, or S_{sj} (S_{gi}) $\neq S_{gi}$, and

$\sigma(S_{gi},S_{gi}) = |S_{gi}|$

The support of tree clusters by data can be measured using the bootstrap technique described in Felsenstein (1985, Evolution 39:783-791).

In an embodiment of the invention, the human antiquitin gene was identified using phylogenetic analysis. The aldehyde dehydrogenase gene family in humans can be subdivided into at least ten ancient subtrees characterized by different functions of corresponding proteins. These genes probably arose from a series of gene duplications of an ancestral gene which took place before the divergence of a common ancestor of Eukaryotes and Eubacteria.

The aldehyde dehydrogenase gene cluster is highlighted in Figure 6 which shows the original tree of ALDH sequences, the circled area indicating a sequence cluster where bacterial (*Bacillus subtilis*), plant (*Brassica napus*), and nematode (*Caenorhabditis elegans*) ortholog is present, but a human ortholog is not known. A random screening of cDNA libraries showed that a human ortholog, referred to as antiquitin, does exist. Figure 7 shows the same gene tree as in Figure 6 with an additional human protein referred to as antiquitin present in the tree.

In yet another embodiment of the invention, a human ortholog of the murine Max-interacting transcriptional repressor Mad3 was identified through phylogenetic analysis of a gene family. The gene tree was constructed as follows. The protein sequences of known members of the *Mad* gene family were extracted from GenBank database. The extracted sequences were aligned using multiple alignment program CLUSTALW running on Sun SPARC station. Redundant and non-homologous sequences as well as distant homologs from *S. cerevisiae*, *C. elegans*, *D. melanogaster* etc. were removed from the alignment. The refined set of sequences were realigned with CLUSTALW and a gene tree as presented in Figure 18A was computed. To identify a human ortholog of the Mad3 protein, a human dbEST at NCBI was searched with program TBLASTN using mouse Mad3 protein sequences as a query. Two highly homologous ESTs were identified and are presented in Figure 17A. To obtain a complete coding sequence a search was

conducted to obtain overlapping sequences in dbEST. The search for overlapping sequences was performed using the program Iterate with EST Zs77e55.rl (gb/AA278224) as the search query. The search identified a single overlapping sequence. The search for overlapping sequences was performed using program Iterate with EST zs77e55.rl (gb/AA278224) serving as a query. The search returned a single overlapping sequence, namely HUMGS0012279 (dbj/C02407), thus showing that the two EST sequences found during the initial TBLASTIN search belong to the same gene. The complete sequence of the gene was assembled from the two ESTs using commercially available sequence assembly program SeqMan11(DNASTAR Inc., WI). The nucleotide sequence of the human Mad3 gene is presented in Figure 17B. The deduced amino acid sequence of which is presented in Figure 17C. The complete DNA sequence is also shown.

The present invention relates to nucleic acid molecules encoding the human Mad3 protein shown in Figure 17C. The invention also relates to nucleic acid molecules that hybridize to the nucleic acid molecule of Figure 17B under conditions of high stringency and encode a Mad3 protein. By way of example and not limitation, procedures using such conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 hours to overnight at 65°C in buffer composed of 6x SSC, 50mM Tris-HCl (pH7.5), ImM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA and 500 mg/ml denatured salmon sperm DNA. Filters are hybridized for 48 hours at 65°C in prehybridization mixture containing 100 mg/ml denatured salmon sperm DNA and 5-20 x 10^6 CpM of ^{32}P-labeled probe. Washing of filters is done at 37°C for 1 hour in a solution containing 2x SSC, 0.01% PVP, 0.01% Ficoll and 0.01% BSA. This is followed by a wash in 0.1x SSC at 50°C for 45 minutes before autoradiography. Other conditions of high stringency which may be used are well known in the art.

5.5. SIMULATION AND HYPOTHESIS TESTING

The simulation and hypothesis testing methods of the invention, described in the subsections below, utilize specialized databases of gene/protein structures and interactions for identifying potentially undiscovered members of

multigene families through comparisons of regulatory networks for different species, searching expressed sequence tag (EST) databases, and simulation of regulatory cascades.

5.5.1. GENE DISCOVERY THROUGH ANALYSIS OF REGULATORY NETWORKS

The present invention provides a method for identifying undiscovered genes through comparisons of regulatory networks for different species where functionally similar regulatory systems are conserved. The amount of information available concerning regulatory genes and/or proteins in different organisms and their functional relationships allows one to reconstruct and compare regulatory networks. Since in most cases, the knowledge of all genes involved in almost any particular regulatory system is incomplete, a comparison of homologous networks within the same organism and between different species permits the identification of genes absent in a system under comparison.

The identified genes, being part of a regulatory network, are implicated as potentially contributing to a phenotype of a disease associated with the system under analysis. Using the methods of the present invention these putative disease genes can be cloned, mapped and analyzed for mutations directly, thereby omitting the expensive and time-consuming steps of positional cloning and sequencing of genomic regions. Gene discovery by analysis of regulatory networks is outlined in Figure 8. The analysis is initiated starting with a biological system (*e.g.*, signaling pathway of genes involved in Bcl-2-regulated apoptosis in lymphocytes), a single gene (e.g., Bcl-2) or a gene family (e.g., caspases).

Initially, a specialized database is generated for comparison of regulatory networks between different species. For example, starting with a single candidate gene in a single species, a typical iteration in this process begins with identification of all known proteins and genes that are upstream and downstream with respect to it in regulatory hierarchies and the reconstruction of a network of interacting genes and proteins. Next, for each protein, a set of key domains and motifs is identified and this information is used to search for related proteins in humans and

other species. The identified sequences are compared and for each pair of sequences showing similarity above a certain threshold, a similarity object is generated. A similarity object is generated if two sequences, nucleotide or amino acid, show significant similarity in database searches (p value < 0.001). The object retains the following information: (i) reference to similar substances *i.e.*, genes or proteins; (ii) significance of the similarity, similarity score and percent of identity; and (iii) coordinates of the similarity region within two compared sequences. "Orthology objects" constitute a subset of "similarity objects" which satisfies one additional requirement, *i.e.*, that two similar sequences should be identified as orthologs by the tree-based algorithm described above. In identifying orthologs, if gene A is orthologous to gene B, and gene B is orthologous to gene C, gene A is necessarily orthologous to gene C.

In a specific embodiment of the invention, for each species under analysis, orthologous proteins or genes are identified. In a further embodiment of the invention, small orthologous molecules participating in a regulatory network for two or more species may also be identified. Where proteins, genes, or molecules are orthologs, the action of the protein, gene or molecule between species may be interchangeable. If more than two species are involved in the analysis, subtrees of orthologous substances and subtrees of orthologous actions are identified.

Once orthologous genes, proteins or molecules are identified in two or more species, by forming a reconciled tree, for example, a set of orthologous or paralogous regulatory networks can be analyzed and visualized using graph theory where arcs represent actions and vertices represent substances. Thus, the method of the invention may further comprise the following steps: (i) superimposing the orthologous regulatory networks from two or more species and searching for the actions (arcs) and substances (vertices) in the homologous networks that are represented in some taxa but absent in others; (ii) superimposing paralogous regulatory networks from the same taxa and searching for paralogous genes that are missing in some taxa; and (iii) computing a general regulatory network that summarizes common regulatory sequence relationships known for more than one species.

In a specific embodiment of the invention a set of regulatory networks from different species, relating to the same biological system, apoptosis, for example, can be analyzed and visualized utilizing the following methods: (i) for each species functional information is collected relating to apoptosis; (ii) using the functional information, regulatory networks for each species comprised of interacting proteins and/or the genes involved in apoptosis are generated; (iii) the sequences of the interacting proteins and genes of each of the regulatory network are compared and for sequences showing similarity above a predetermined threshold range; and (iv) distinguishing between orthologs and paralogs using the methods set forth above.

An analysis similar to that performed using subtrees of sequences may be applied to classify protein functions as orthologous or paralogous actions. A "generalized" regulatory network maybe represented as a network wherein a substance as it occurs in a particular species is substituted with a cluster (i.e., subtree) of orthologous substances among species. In the final step of the analysis the clusters within each species are compared to one another, to identify missing genes.

Figure 11 depicts the regulatory relationships among hypothetical proteins (denoted with Arabic numerals) of hypothetical species A and B. As indicated in Figure 11A, an overlay of regulatory data for two species overlaps, but not completely. As indicated, protein 5 is known only for species B while protein 3 is known only for species A. The proteins in different species denoted with the same numeral are considered orthologous. As indicated, the regulatory relationships between a pair of proteins can be of three different kinds. Figure 9B, 9C, and 9D represent Boolean operations, OR, AND, and XOR, as arcs of the two regulatory relationships depicted in Figure 9A, the same operations being applicable to the set of vertices of the two regulatory relationships.

In some instances, orthologous networks in two distantly related taxa may have the same domains but arrangement of the domains between the related taxa may be different. In such a case, a one-to-one correspondence between orthologous proteins in closely related species has to be substituted with a one-to-many relationship among domains comprised within the proteins. For this purpose, a similarity object may be defined operating on pairs of motifs/domains in two proteins, and substitute pairs of

orthologous proteins with pairs of orthologous domains. After this correction, homologous networks are compared as described above.

Figure 10 is a diagram representing a hypothetical example of defining homologous protein networks in two different species using protein motifs, the diagram showing only two hypothetical proteins (lane 2) for species A and three hypothetical proteins (lanes 1, 3, and 4) for species B. Protein 1 in both species has motifs α and β, protein 2 has motifs δ, ϵ, and ζ, and proteins 3 and 4 have motifs δ and ζ, and ϵ, respectively. The motif analysis indicates that proteins 3 and 4 in species B may collectively perform the same function as protein 2 in species A.

5.5.2 GENE DISCOVERY BASED ON PROTEIN MOTIF/DOMAIN SEARCHES

The present invention provides yet another method for identifying genes that are homologous and perform the same or an analogous function in different species. The method of the invention comprises the following steps: (i) creating a database of sequences which comprise a motif or domain composition of a gene of interest using, for example, HMMER software; and (ii) searching additional databases for expressed sequence tags (ESTs) containing the domains and motifs characteristic for the gene of interest with HMMs of domains and motifs identified in step (i). In yet another embodiment of the invention, sequences may be searched which correspond to nucleotide sequences in an EST database or other cDNA databases using a program such as BLAST and retrieving the identified sequences. In an optional step, for each EST identified, sequence databases can be searched for overlapping sequences for the purpose of assembling longer overlapping stretches of DNA. Once identified, the ESTs can be used to isolate full length nucleotide sequences comprising the gene of interest using methods such as those described in Section 5.4, *infra*.

The general flowchart scheme for gene discovery analysis based on motif/domain search is shown in Figure 11. In a specific embodiment of the invention, the method referred to as the "phylogenetic reflection technique"comprises, first, defining the motif or domain composition of a gene of interest involved in a biological system of interest. Second, protein-coding genes from other species,

including for example yeast and/or nematode genes, that bear a significant similarity to the gene of interest or a specified domain of the corresponding protein are collected. Third, the identified genes are in turn subjected to a "domain analysis" to establish protein motifs which might suggest a function of these genes using, for example, HMMER software. Fourth, the selected genes are in turn used for database searches in EST databases (dbEST) and/or a non-redundant (nr) database to identify unknown genes that are potentially orthologous to the selected yeast and nematode genes. Once identified ESTs having different tumor suppressor domains may be linked using multiple PCR primers. Using routine cloning techniques, well known to those of skill in the art, a full length cDNA representing the gene of interest can be obtained.

Once new genes are identified by domain/motif analysis experimental searches may be carried out to isolate complete coding sequences and evaluate their tissue- and disease-specific expression patterns. In parallel their position with respect to regulatory networks can be identified as described below.

In a specific embodiment of the invention, an apoptosis related human gene was identified using the method described above. As a first step *C. elegans* genes containing either POZ or Kelch domains were identified. A Hidden Markov Model was developed using POZ and Kelch sequences from the *Drosophila* Kelch protein and any identified homologs. The resulting Hidden Marker Model was used to search through the collection of *C. elegans* protein sequences. One of the identified *C. elegans* genes contained a POZ domain, death domain, kinase domain and heat repeat. The presence of both a death domain and a kinase domain suggested that the protein functions as a regulatory protein.

A human EST database was searched using the protein sequence of the identified *C. elegans* gene and two sequences were identified (Figure 14A). A gene tree was computed to determine whether the identified human sequences were orthologs of the *C. elegans* gene. As depicted in Figure 14B, the human EST AA481214 appears to be a true ortholog of the *C. elegans* gene. Figure 14C presents the nucleotide sequence of the identified death domain gene. Figure 14D presents the amino acid sequence of the death domain protein.

The present invention encompasses the nucleic acid molecule of Figure 14C, comprising the sequence of EST AA481214 and proteins encoded by said nucleic acid molecule. The invention also relates to nucleic acid molecules capable of hybridizing to such a nucleic acid molecule under conditions of high stringency. By way of example and not limitation, procedures using such conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 hours to overnight at 65°C in buffer composed of 6x SSC, 50mM Tris-HCl (pH7.5), ImM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA and 500 mg/ml denatured salmon sperm DNA. Filters are hybridized for 48 hours at 65°C in prehybridization mixture containing 100 mg/ml denatured salmon sperm DNA and 5-20 x 10^6 CpM of ^{32}P-labeled probe. Washing of filters is done at 37°C for 1 hour in a solution containing 2x SSC, 0.01% PVP, 0.01% Ficoll and 0.01% BSA. This is followed by a wash in 0.1x SSC at 50°C for 45 minutes before autoradiography. Other conditions of high stringency which may be used are well known in the art.

5.5.3. SIMULATION OF REGULATORY CASCADES

In an embodiment of the invention, an interactive graphical program is utilized for visualizing the scheme of regulatory relationships, "current" states of the substances, and active and inactive actions between pairs of substances. Such a program can be utilized for identification of genes which are associated with a specific disease. Currently, disease associated genes are discovered through positional cloning methods which combine methods of genetics and physical mapping with mutational analysis. The present invention provides a novel method for discovering disease associated genes. For simulating regulatory cascades, it is assumed that the time in a simulated regulatory system advances in discrete "quanta," or periods of time. The "state of substances" of the system for each discrete period of time is computed by: creating a set of substance objects, where a set of interactions between each created substance object is known, an initial state is specified. The time is initially set to zero. All defined actions are observed to confirm that the substances corresponding to the actions (i) exist, and (ii) are in the right initial states. Action is defined by a pair of substances that are in suitable states. The "subject" substance is in the inactive state,

while the "object" substance can be in either active, or inactive, state depending on the action type. For example, the action "dephosphorylation" requires an active phosphatase ("subject" substance) and a phosphorylated substitute protein ("object" substance) in phosphorylated form. If both conditions are satisfied, the action is recorded as in progress. At termination, the substances must change their states as specified by the action. On each following "quantum" of time, the simulation proceeds in the same way while maintaining the "bookkeeping" of the remaining time for each action and the remaining lifespan of each substance. The simulation stops when there are no more active actions available. The program allows editing of the properties of the objects, changing the scale and focus of the visualized simulation, and experimenting with the systems output.

In a specific embodiment of the invention a "knock out" of a gene can be simulated to model the regulatory system that normally includes hypothetical gene A. One of the typical questions related to the gene knock out is how does the knock out affect a biological pathway of interest. A hypothetical example of evaluating the impact of a knock out of hypothetical gene A on the expression of a hypothetical gene B is shown in Figure 12. The answer to such a question could be "gene B will be inhibited" or "gene B will be induced" or "no effect".

In the practice of the present invention, a simple algorithm involving multiplication of gene interaction "signs" along the shortest pathway between the genes can be used to determine the outcome. The algorithm involves the following steps: (i) identification of the shortest non-oriented pathway connecting genes A and B involved in a pathway of interest; (ii) assigning sign "-" to gene A since it is knocked out and taking this sign as the initial sign value; (iii) moving along the shortest pathway between genes A and B, multiplying the current value of the sign with the sign of the next arc, where "-" stands for inhibition, "+" stands for induction or activation, and "0" stands for the lack of interaction between two proteins in the specified direction; (iv) determining if the final result of multiplication is "0", if so eliminating the zero arc and trying to find the shortest oriented bypass pathway between A and B in the remaining network; otherwise stop. The final value of the sign at the moment of arriving at vertex B would indicate the most likely effect of the

knock out of gene A which can be any one of the following: inhibition of gene B, induction/activation of gene B, or none. In addition to the "electronic knock out", an "electronic knock in" of a particular gene can be simulated. In such a computer simulation, the artificial addition of a gene and its effect on a regulatory system may be analyzed.

5.6. IDENTIFICATION AND ISOLATION OF NOVEL GENES

The present invention relates to identification of novel genes, i.e., missing orthologs or paralogs, and the isolation of nucleic acid molecules encoding novel genes. In a specific embodiment, a nucleic acid molecule encoding a missing ortholog or paralog can be isolated using procedures well known to those skilled in the art (See, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York Glover, D.M. (ed.), 1985, DNA Cloning: A Practical Approach MRL Press, Ltd., Oxford, U.K. Vol. I, II.).

For example, genomic and/or cDNA libraries may be screened with labeled DNA fragments derived from a known ortholog or paralog from a specific species and hybridized to the genomic or cDNA libraries generated from a different species. For cross species hybridization, low stringency conditions are preferred. For same species hybridization, moderately stringent conditions are preferred. Any eukaryotic cell potentially can serve as the nucleic acid source for the molecular cloning of the gene of interest. The DNA may be obtained by standard procedures known in the art from cloned DNA (e.g., a DNA "library"), by cDNA cloning, or by the cloning of genomic DNA, or fragments thereof, purified from the desired cell.

By way of example and not limitation, procedures using conditions of low stringency are as follows (see also Shilo and Weinberg, 1981, Proc. Natl. Acad. Sci. USA 78:6789-6792; and Sambrook et al. 1989, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory Press, Cold Spring harbor, New York): Filters containing DNA are pretreated for 6 h at 40°C in a solution containing 35% formamide, 5X SSC, 50 mM Tris-HC1 (pH 7.5), 5 mM EDTA, 0.1% PVP, 0.1% Ficoll, 1% BSA, and 500 mg/ml denatured salmon sperm DNA. Hybridizations are

carried out in the same solution with the following modifications: 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml salmon sperm DNA, 10% (wt/vol) dextran sulfate, and 5-20 X 10^6 cpm ^{32}P-labeled probe is used. Filters are incubated in hybridization mixture for 18-20 h at 40°C, and then washed for 1.5 h at 55°C in a solution containing 2X SSC, 25 mM Tris-HC1 (pH 7.4), 5 mM EDTA, and 0.1% SDS. The wash solution is replaced with fresh solution and incubated an additional 1.5 h at 60°C. Filters are blotted dry and exposed for autoradiography. If necessary, filters are washed for a third time at 65-68°C and reexposed to film. Other conditions of low stringency which may be used are well known in the art (*e.g.*, as employed for cross species hybridizations).

In another specific embodiment, a nucleic acid which is hybridizable to a nucleic acid under conditions of moderate stringency is provided. For example, but not by way of limitation, procedures using such conditions of moderate stringency are as follows: filters containing DNA are pretreated for 6 h at 55°C in a solution containing 6X SSC, 5X Denhart's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA. Hybridizations are carried out in the same solution and 5-20 X 10^6 CpM ^{32}P- labeled probe is used. Filters are incubated in the hybridization mixture for 18-20 h at 55°C, and then washed twice for 30 minutes at 60°C in a solution containing 1X SSC and 0.1% SDS. Filters are blotted dry and exposed for autoradiography. Other conditions of moderate stringency which may be used are well-known in the art. Washing of filters is done at 37°C for 1 h in a solution containing 2X SSC, 0.1% SDS.

For expression cloning (a technique commonly used in the art), an expression library is constructed. For example, mRNA is isolated from the cell type of interest, cDNA is made and ligated into an expression vector (*e.g.*, a bacteriophage derivative) such that it is capable of being expressed by a host cell (*e.g.*, a bacterium) into which it is then introduced. Various screening assays can then be used to select for the expressed gene product of interest based on the physical, chemical, or immunological properties of its expressed product. Such properties can be deduced from the properties of the corresponding orthologs from other species.

In another embodiment, polymerase chain reaction (PCR) can be used to amplify the desired sequence from a genomic or cDNA library. To isolate orthologous or paralogous genes from other species, one synthesizes several different degenerate primers, for use in PCR reactions. In a preferred aspect, the oligonucleotide primers represent at least part of the gene comprising known ortholog or paralog sequences of different species. It is also possible to vary the stringency of hybridization conditions used in priming the PCR reactions, to allow for greater or lesser degrees of nucleotide sequence similarity between the known nucleotide sequences and the nucleic acid homolog being isolated.

Synthetic oligonucleotides may be utilized as primers to amplify by PCR sequences from a source (RNA or DNA), preferably a cDNA library, of potential interest. PCR can be carried out, *e.g.*, by use of a Perkin-Elmer Cetus thermal cycler and a thermostable polymerase, *e.g.*, Amplitaq (Perkin-Elmer). The nucleic acids being amplified can include mRNA or cDNA or genomic DNA from any eukaryotic species. After successful amplification of a segment of a the gene of interest, that segment may be molecularly cloned and sequenced, and utilized as a probe to isolate a complete cDNA or genomic clone.

Once identified and isolated the gene of interest can then be inserted into an appropriate cloning vector for amplification and/or expression in a host. A large number of vector-host systems known in the art may be used. Possible vectors include, but are not limited to, plasmids and modified viruses, but the vector system must be compatible with the host cell used. Such vectors include, but are not limited to, bacteriophages such as lambda derivatives, or plasmids such as pBR322 or pUC plasmid derivatives or the Bluescript vector (Stratagene). The insertion into a cloning vector can, for example, be accomplished by ligating the DNA fragment into a cloning vector which has complementary cohesive termini.

6. EXAMPLE: USE OF SPECIALIZED DATABASES FOR IDENTIFICATION OF NOVEL GENES

To test the method of using databases for gene discovery, protein sequence and domain/motif databases specific to two overlapping functional

groupings of proteins: (i) proteins known to be tumor suppressors, and (ii) proteins implicated in apoptosis in animals were developed.

6.1 APOPTOSIS GENE DISCOVERY METHOD

Identification of a putative apoptosis-related human gene began with an identification of all genes in *C. elegans* that contained either a POZ or kelch domain. A subset of these genes is shown in Figure 13. Hidden Markov Models (HMM) for the POZ and Kelch domains were built as follows. Starting with POZ and kelch sequences from the *Drosophilia* kelch protein (gi|577275) homologs were identified in other protein sequences using the BLASTP program. The resulting sequences showing significant similarity (e-value less than 0.001) were aligned using CLUSTALW program and the alignments were used to build Hidden Markov Models with HMMER-2 package (Krogh et al., 1995, :http://hmmer.wustl.edu/). A computer printout listing of HMM models of tumor suppressors appears as a Microfiche H to the present specification. (See, http://hmmer.wustl.edu; Chapter 2, which is incorporated by reference herein in its entirety, for a detailed description of HMM models)

The resulting models were used to search through a database collection of *C.elegans* protein sequences. The domain structures of proteins having either a POZ or kelch domain were identified using existing collections of protein domains (e.g., see http://blocks.fhcrc.org/blocks/blocks release.html, http://coot.embl-heidelberg.de/SMART/, http://www.motif.genome.ad.jp/). One of the unannotated protein-coding genes of *C. elegans* (corresponding protein accession number gi|1132541, see Figure 11) appeared to include a POZ domain, death domain, kinase domain, and heat repeat. A death domain is characteristic for the apoptosis system and a kinase domain indicates that the protein is likely to participate in phosphorylation of other proteins. The presence of these particular domains suggests that this protein is serving as a regulatory protein.

Using the protein sequence of gi|1132541, the database of human EST sequences was searched and a number of partial human cDNA sequences representing potential human orthologs or paralogs of the *C.elegans* gi|1132541 were identified.

The two closest human sequences, AA481214 and W51957, are depicted in Figure 14A. To determine whether the identified human sequences were orthologs or paralogs to the gi|1132541 gene of *C. elegans*, a gene tree (Saito and Nei, 1997, Molecular Biol. Evol. 4:406-425) was computed. The gene tree was generated using homologous genes identified with a BLASTP search against NCBI non-redundant database, using the human EST AA481214 sequence as a query. The resulting tree indicates that the identified human EST AA481214 represents a true ortholog of the *C.elegans* gene gi|1132541 (Figure 14B). The nucleotide sequence of the death domain protein is shown in Figure 14C, as well as the deduced amino acid sequence presented in Figure 14D.

6.1.2 APOPTOSIS GENE DISCOVERY METHOD

As a first step in identifying a novel gene involved in apoptosis, a comprehensive set of articles describing the system of apoptosis/programmed cell death in different species was compiled using the keyword "apoptosis". By analyzing the articles, information on regulatory pathways characterizing this system in different species, *i.e.*, *C. elegans*, mouse, fruit fly, chicken, and human, was extracted. The regulatory information was stored as a collection of schemes produced in PowerPoint (Microsoft). Figure 4 shows a set of keywords defining proteins involved in apoptosis pathways. The keywords were used to generate a specialized sequence database, referred to as Apoptosis3, utilizing the PsiRetriever program for extraction of proteins from the all-inclusive non-redundant GenBank database (NCBI). Using program PsiRetriever, sequences from the non-redundant (NCBI) database of protein sequences, were retrieved and stored as a FASTA file. The FASTA file was then converted into binary blast database using program FORMATDB from the BLAST suit of programs.

Genomic and cDNA sequences located in the region of human chromosome 13q were compared with the Apoptosis3 database using BLASTALL program from BLAST program complex. This region of the human genome is associated with Chronic Lymphocytic Leukemia (CLL). The comparison revealed significant similarity between a CLL region open reading frame and the mouse RPT1

protein (sp|P15533|RPT1) (Figure 13). Analysis of regulatory functions of RPT1 in the mouse reveals that this gene functions as a repressor of the interleukin 2 receptor (IL-2R) gene. When the RPT1 gene is knocked out, the regulatory effect is manifested as a block of the apoptotic pathway in T lymphocytes resulting in an accumulation of T lymphocytes in blood. This result is consistent with aberrations observed in CLL, namely abnormal accumulation of B-cells in the blood (Trentin L. et al., 1997, Leuk. Lymphoma 27:35-42) and mutations in the human RPT1 gene play a role in development of CLL.

6.1.3 EXAMPLE: A DISCOVERY OF A HUMAN ORTHOLOG OF THE MURINE MAX-INTERACTING TRANSCRIPTIONAL REPRESSOR

The family of *Myc* proto-oncogenes encodes a set of transcription factors implicated in regulation of cell proliferation, differentiation, transformation and apoptosis. C-*Myc* null mutations result in retarded growth and development of mouse embryos and are lethal by 9-10 day of gestation. In contrast, overexpression of *Myc* genes inhibits cell differentiation and leads to neoplastic transformation. Moreover, deregulation of *Myc* expression by retroviral transduction, chromosomal translocation or gene amplification is linked to a broad range of naturally occurring tumors in humans and other species.

Another protein, called *Max*, is an obligatory heterodimeric partner for *Myc* proteins in mediating their function as activators of transcription during cell cycle progression, neoplastic transformation and programmed cell death (apoptosis). In order to make an active transcription factor the *Myc* proteins must form heterodimers with *Max* protein. This interaction with *Max* protein is necessary for specific binding of *Myc* with CACGTG box (or related E-boxes) on DNA and for activation of promoters located proximal to the binding sites.

Besides the *Myc* family of transcription factors, the *Max* protein forms complexes with another family of so-called *MAD* proteins: *Mxi1*, *MAD1*, *MAD3* and *MAD4*. Whereas *Myc*:*Max* complexes activate transcription, *MAD*:*Max* complexes work in an opposite way repressing the transcription through the same E-box binding

sites and apparently antagonize *Myc*-mediated activation of the same set of target genes.

During tissue development a shift from *Myc*:*Max* to *MAD*:*Max* complexes occurs coincidentally with the switch from cell proliferation to differentiation. The switch in heterocomplexes is thought to reflect a switch from activation to repression of common genes leading to cessation of proliferation, exiting the cell cycle and the beginning of cell differentiation. In differentiating neurons, primary keratinocytes, myeloid cell lines and probably other tissues the expression of different *MAD*:*Max* complexes appear in sequential order during the transition from cell proliferation to differentiation. The *MAD3* expression appears first and it is restricted to proliferating cells prior to differentiation where it is co-expressed with two different member of *Myc* family, c-*Myc* or N-*Myc*. *Mxi1* transcripts are detected in proliferating and differentiating cells whereas *MAD1* and *MAD4* were confined to post-mitotic cells. Because *Myc* expression is not always downregulated in post-mitotic cells, co-expression of *Myc* and *MAD* genes may result in competition for *Max* heterodimers thus providing promoting or inhibitory effect on cell proliferation.

The gene expression patterns, along with ability of Mad proteins to suppress *Myc*-dependent transformation, are consistent with a potential function of Mad genes as tumor suppressors. This view is supported by the fact that allelic loss and mutations were detected at the *Mxi1* locus in prostate cancers (Eagle et al., 1995 Nat Genet 9:249-55). Cloning of the murine proteins *Mad3* and *Mad4* as well as their relation to *Max* signaling network was described by Hurlin (Hurlin PJ, et al., 1995, EMBO J. 14:5646-59) and Queva (Queva et al. 1998 Oncogene 16:967-977). Human orthologs of *Mad4*, *Mad1* and *Mxi1* are known.

In this example, the discovery of an unknown human ortholog of *Mad3* protein found "*in silico*," by means of phylogenetic analysis of known mouse and human members of the *Mad* gene family and database searches is described. Since the function of murine *Mad3* as a *Max*-interacting transcriptional repressor of *Myc*-induced neoplastic transformation is well described, we can assign the same function to its human ortholog.

The gene tree shown in the Figure 20 was constructed in the following way. The protein sequences of known members of *Mad* gene family were extracted from GenBank database using NCBI Entrez keyword searches. The extracted sequences were aligned using multiple alignment program Clustalw running on Sun SPARC station. The quality of the multiple alignment was checked using program HitViewer Iterate (A. Rzhetsky, available upon request) and the redundant, non-homologous sequences as well as distant homologs from *S. cerevisiae, C. elegans, D. melanogaster* etc. were removed from the alignment. The refined set of sequences was realigned with Clustalw and a gene tree as presented in Figure 15A was computed from the alignment using program NJBOOT (http://genome6.cpmc.columbia.edu // andrey) running on Sun SPARC station and viewed with program TreeView (http://genome6.cpmc.columbia.edu // andrey).

The tree presented in Fig.19A clearly shows the relationships between three known mouse genes and their two human homologs. Attempts to find a missing human ortholog of the mouse *Mad3* gene in protein non-redundant database at NCBI using BLAST search did not identify any human homologs other than sequences that were already present on the tree, confirming the absence of a known human ortholog for Mad3 protein in the database.

In order to identify a human ortholog of the Mad3 protein, a human dbEST at NCBI was searched with program TBLASTN using Mad3 protein sequence as a query. Two EST were identified and are shown in Figure 17A.

Due to the nature of dbEST database this search produced only partial sequences of potential candidate genes. To obtain complete coding sequences (complete cds) of the genes, a search was conducted to obtain overlapping sequences in dbEST. The search for overlapping sequences was performed using the program Iterate with EST zs77e55.r1 (gb|AA278224) serving as a query. The search returned a single overlapping sequence, namely HUMGS0012279 (dbj|C02407), thus indicating that the two EST sequences found during the initial TBLASTN search belong to the same gene.

The complete sequence of the gene was assembled from the two ESTs using commercially available sequence assembly program SeqManII (DNASTAR Inc.,

WI). The nucleotide sequence of the human *Mad*3 gene is presented in Figure 17B. The deduced amino acid sequence of the gene is presented in Figure 17C. The translated sequence consists of 206 amino acid residues 81% of which are identical to mouse Mad3 protein. The alignment of human and mouse Mad3 proteins shown below was made using BLAST server at NCBI and is presented in Figure 17C.

Multiple alignment of the new sequence with sequences of known Mad proteins was made using Clustalw and viewed with the HitViewer. A gene tree was computed from this alignment using NJBOOT. Multiple alignment of the new sequence with sequences of known Mad proteins (Figure 17C) along with its position on gene tree (Figure 18B) shows that this new human gene found by the approach described above belongs to the family of Mad proteins and is the ortholog of mouse Mad3.

The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention, and functionally equivalent methods and components are within the scope of the invention. Indeed, various modifications of the invention, in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

Various publications are cited herein, the contents of which are hereby incorporated by reference in their entireties.

CLAIMS

1. A method for identifying a novel nucleic acid molecule encoding a protein of interest comprising:

(i) selecting a specific protein from a first species involved in a regulatory network of interest;

(ii) identifying known proteins that act upstream and downstream in the regulatory network of interest with respect to the specific protein selected;

(iii) constructing the regulatory network of interest from the proteins identified in step (ii);

(iv) for each identified protein, select a domain or motif and search by homology for related proteins in a second species, wherein a related protein is defined as a protein having a homologous domain or motif;

(v) producing a regulatory network for the second species, wherein said regulatory network incorporates the identified related proteins;

(vi) comparing the regulatory network from the first species to the regulatory network of said second species;

(v) identifying a protein present in a regulatory network for one species but absent in the regulatory network of the other species; and

(vi) isolating a nucleic acid molecule encoding the protein identified in step (v) in the species in which it is missing.

2. The method of Claim 1 wherein the nucleic acid molecule encodes human protein.

3. The method of claim 1 wherein the related proteins are orthologs.

4. The method of claim 1 wherein the regulatory pathway is involved in apoptosis.

5. The method of claim 1 wherein the specific protein from the first species is involved in tumor suppression.

6. A method for identifying the affect of a gene knockout on a regulatory pathway comprising the following steps:

(i) identification of the shortest non-oriented pathway connecting two gene products;

(ii) assigning an initial sign value of "-" to the knockout since the knockout gene product is inactive;

(iii) moving along the shortest pathway between the two gene products multiplying the sign with the sign of the next gene product in the pathway, wherein "-" stands for inhibition, "+" stands for induction or activation, and "0" stands for the lack of interaction between two proteins in the specified direction; and

(iv) determining the final sign at the end of the pathway, wherein "-" indicates inhibition and "+" indicates induction or activation of the pathway.

7. A method for identifying a novel nucleic acid molecule encoding a protein of interest comprising:

(i) selecting a gene of interest and searching a database for homologous sequences;

(ii) aligning the homologous sequences identified in step (*i*);

(iii) constructing a gene tree using the sequence alignment;

(iv) constructing a species tree;

(v) imputing the species tree and gene tree into an algorithm which integrates the species tree and the gene tree into a reconciled tree; and

(vi) identifying orthologous genes present in one species but missing in another.

8. The method of claim 7 wherein the following algorithm is used to integrate the species tree and the gene tree into a reconciled tree:

(i) computing the similarity $\sigma(S_{gi},S_{sj})$ for each pair of interior nodes from trees T_g and T_s,

(ii) finding the maximum $\sigma(S_{gl},S_{sj})$;

(iii) saving S_{gi} as a new cluster of orthologs, save $\{S_{gi}\}$ - $\{S_{sj}\}$ as a set of species that are likely to have gene of this kind (or lost it in evolution);

(iv) eliminating S_{gi} from T_g; $T_g := T_g \backslash S_{gi}$;

(v) repeating step (ii)-(iv) until T_g is non-empty.

9. A method for identifying a novel gene comprising the following steps:

(i) defining a motif or domain composition of a gene of interest;

(ii) searching for sequences which correspond to nucleotide sequences in an expression sequence tag database or other cDNA databases using a program such as BLAST and retrieving the identified sequences;

(iii) searching additional databases for expressed sequence tags containing the domains and motifs characteristic for the gene of interest with Hidden Markov Model of domains and motifs identified in step (i);

(iv) identifying nucleotide sequences comprising the gene of interest.

10. The method of claim 9 further comprising using each identified expression sequence tag to search sequence databases for overlapping sequences for the purpose of assembling longer overlapping stretches of DNA.

11. A method for extracting information on interactions between biological entities from natural-language text data, comprising:

(i) parsing the text data to determine the grammatical structure of the text data ;and

(ii) regularizing the parsed text data to form structured word terms.

12. The method according to claim 11, further comprising preprocessing the data prior to parsing, with preprocessing comprising the step of identifying biological entities.

13. The method according to claim 11, further comprising referring to an additional parameter which is indicative of the degree to which subphrase parsing is to be carried out.

14. The method according to claim 11, wherein said parsing step further comprises segmenting the text data by sentences.

15. The method according to claim 11, wherein said parsing step further comprises:

segmenting the text data by sentences; and

segmenting each of the sentences at identified words or phrases.

16. The method according to claim 11, wherein said parsing step further comprises:

segmenting the text data by sentences; and

segmenting each of the sentences at a prefix.

17. The method according to claim 11, wherein said parsing step further comprises skipping undefined words.

18. The method according to claim 11, wherein said parsing step further comprises:

identifying one or more binary actions and their relationships; and

identifying one or more arguments associated with the actions.

19. The method according to claim 11, further comprising performing error recovery when parsing of the text data is unsuccessful.

20. The method according to claim 19, wherein said error recovery step comprises:

segmenting the text data; and

analyzing the segmented text data to achieve at least a partial parsing of the unsuccessfully parsed text data.

21. The method according to claim 11, wherein said tagging step comprises providing the structured data component in a Standard Generalized Markup Language (SGML) compatible format.

22. A computer system for extracting information on biological entities from natural-language text data, comprising:

(i) means for parsing the natural-language text data; and

(ii) means for regularizing the parsed text data to form structured word terms.

23. The system according to claim 22, further comprising means for preprocessing the data prior to parsing, with the preprocessing means comprising identifying biological entities.

24. The system according to claim 22, further comprising means for referring to an additional parameter which is indicative of the degree to which subphrase parsing is to be carried out.

25. The system according to claim 22, wherein said parsing means further comprises means for segmenting the text data by sentences.

26. The system according to claim 22, wherein said parsing means further comprises:

means for segmenting the text data by sentences; and

means for segmenting each of the sentences at identified words or phrases.

27. The system according to claim 22, wherein said parsing means further comprises:

means for segmenting the text data by sentences; and

means for segmenting each of the sentences at a prefix.

28. The system according to claim 22, wherein said parsing means further comprises means for skipping undefined words.

29. The system according to claim 22, wherein said parsing means further comprises:

means for identifying one or more binary actions and their relationships; and

means for identifying one or more arguments associated with the actions.

30. The system according to claim 22, further comprising means for performing error recovery when parsing of the text data is unsuccessful.

31. The system according to claim 22, wherein said error recovery means comprises:

means for segmenting the text data; and

means for analyzing the segmented text data to achieve at least a partial parsing of the unsuccessfully parsed text data.

32. The system according to claim 22, wherein said tagging means comprises means for providing the structured data component in a Standard Generalized Markup Language (SGML) compatible format.

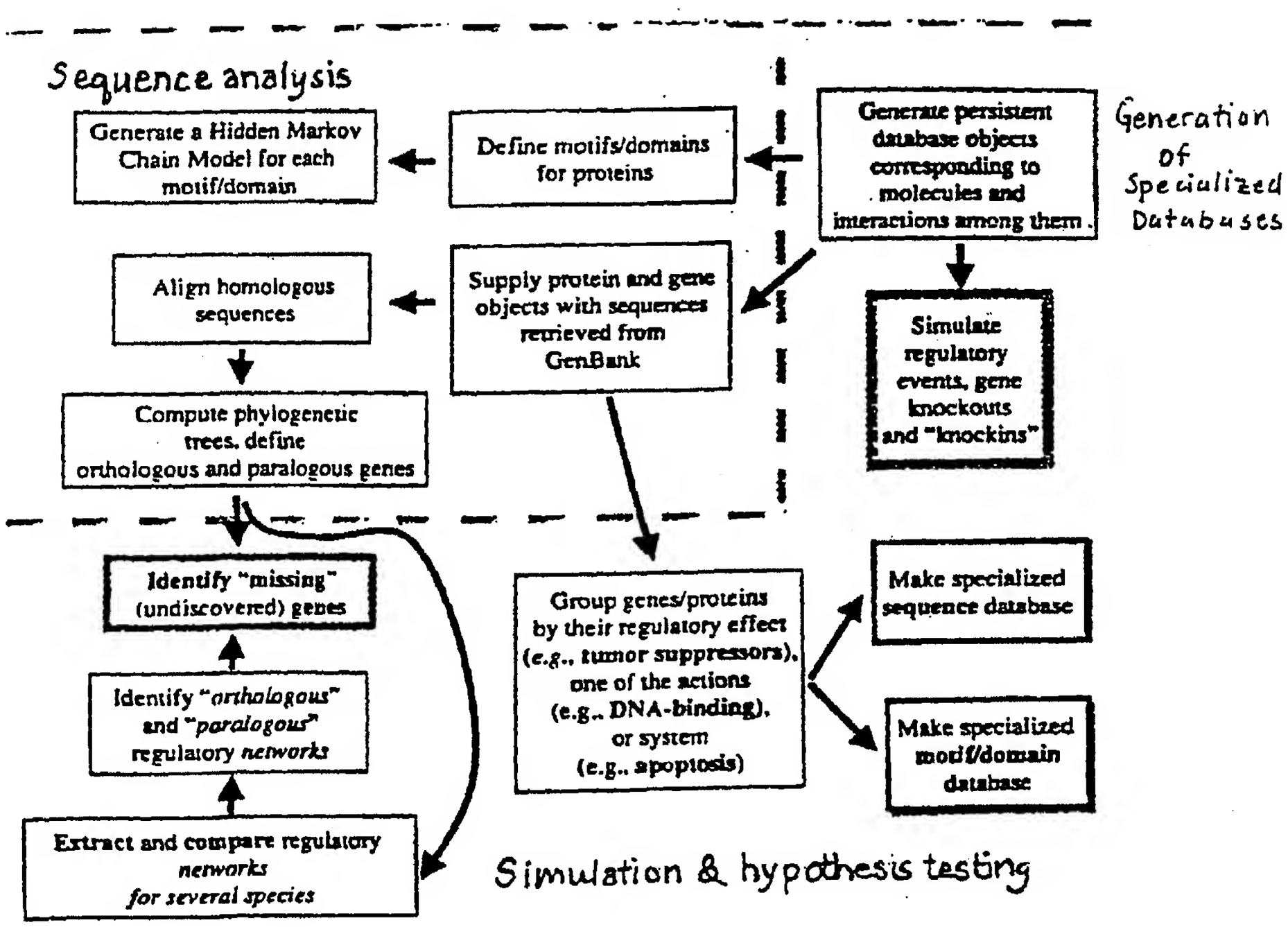

Sequence analysis
Generate a Hidden Markov Chain Model for each motif/domain
Define motifs/domains for proteins
Generate persistent database objects corresponding to molecules and interactions among them
Generation of Specialized Databases
Align homologous sequences
Supply protein and gene objects with sequences retrieved from GenBank
Simulate regulatory events, gene knockouts and "knockins"
Compute phylogenetic trees, define orthologous and paralogous genes
Identify "missing" (undiscovered) genes
Identify "orthologous" and "paralogous" regulatory networks
Extract and compare regulatory networks for several species
Group genes/proteins by their regulatory effect (e.g., tumor suppressors), one of the actions (e.g., DNA-binding), or system (e.g., apoptosis)
Make specialized sequence database
Make specialized motif/domain database
Simulation & hypothesis testing

FIGURE 1

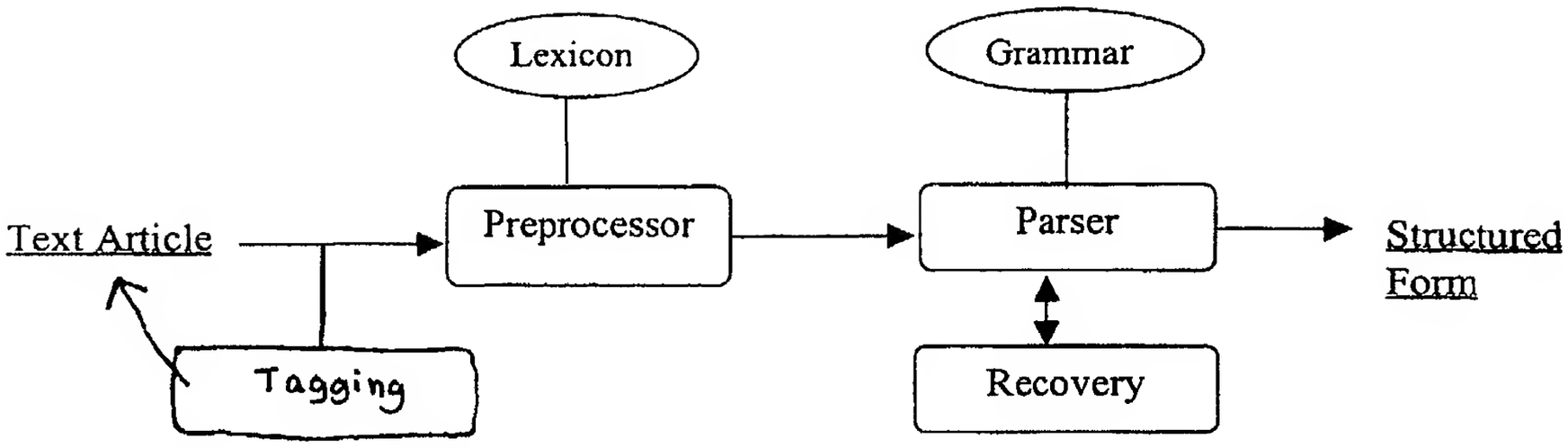

Lexicon
Grammar
Text Article
Preprocessor
Parser
Structured Form
Tagging
Recovery

Figure 2

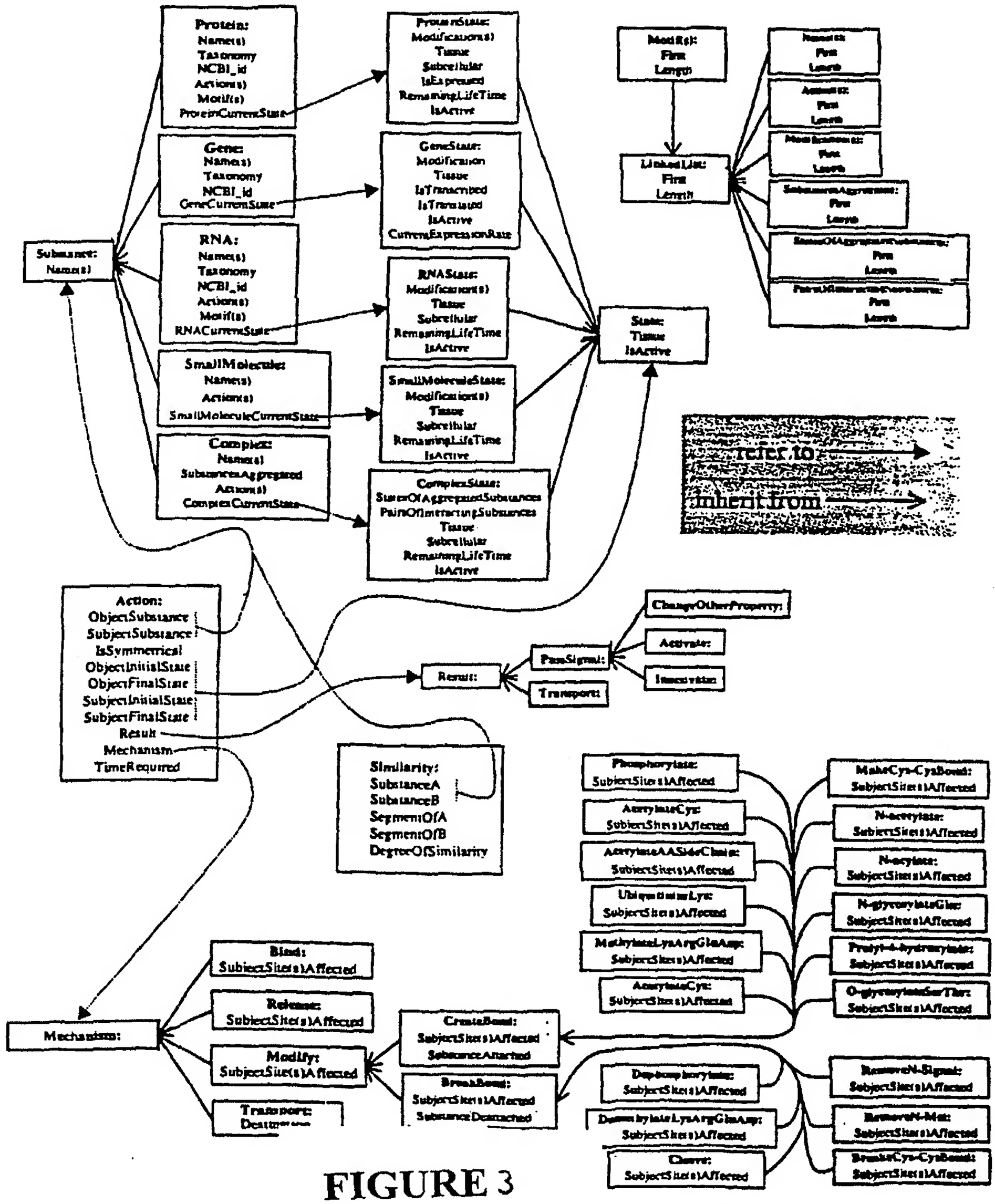

Protein:
Name(s)
Taxonomy
NCBI_id
Action(s)
Motif(s)
ProteinCurrentState
Gene:
Name(s)
Taxonomy
NCBI_id
GeneCurrentState
RNA:
Name(s)
Taxonomy
NCBI_id
Action(s)
Motif(s)
RNACurrentState
SmallMolecule:
Name(s)
Action(s)
SmallMoleculeCurrentState
Complex:
Name(s)
SubstancesAggregated
Action(s)
ComplexCurrentState
Substance:
Name(s)
ProteinState:
Modification(s)
Tissue
Subcellular
IsExpressed
RemainingLifeTime
IsActive
GeneState:
Modification
Tissue
IsTranscribed
IsTranslated
IsActive
CurrentExpressionRate
RNAState:
Modification(s)
Tissue
Subcellular
RemainingLifeTime
IsActive
SmallMoleculeState:
Modification(s)
Tissue
Subcellular
RemainingLifeTime
IsActive
ComplexState:
StatesOfAggregatedSubstances
PairsOfInteractingSubstances
Tissue
Subcellular
RemainingLifeTime
IsActive
Motif(s):
First
Length
LinkedList:
First
Length
State:
Tissue
IsActive
refer to
inherit from
Action:
ObjectSubstance
SubjectSubstance
IsSymmetrical
ObjectInitialState
ObjectFinalState
SubjectInitialState
SubjectFinalState
Result
Mechanism
TimeRequired
Result:
PassSignal:
Transport:
ChangeOtherProperty:
Activate:
Inactivate:
Similarity:
SubstanceA
SubstanceB
SegmentOfA
SegmentOfB
DegreeOfSimilarity
Mechanism:
Bind:
SubjectSite(s)Affected
Release:
SubjectSite(s)Affected
Modify:
SubjectSite(s)Affected
Transport:
CreateBond:
SubjectSite(s)Affected
SubstanceAttached
BreakBond:
SubjectSite(s)Affected
SubstanceDetached
Phosphorylate:
SubjectSite(s)Affected
AcetylateCys:
SubjectSite(s)Affected
AcetylateAASideChain:
SubjectSite(s)Affected
Ubiquitinate Lys:
SubjectSite(s)Affected
MethylateLysArgGlnAsp:
SubjectSite(s)Affected
AcetylateCys:
SubjectSite(s)Affected
MakeCys-CysBond:
SubjectSite(s)Affected
N-acetylate:
SubjectSite(s)Affected
N-acylate:
SubjectSite(s)Affected
N-glycosylateGln:
SubjectSite(s)Affected
Prolyl-4-hydroxylate:
SubjectSite(s)Affected
O-glycosylateSerThr:
SubjectSite(s)Affected
Dephosphorylate:
SubjectSite(s)Affected
DemethylateLysArgGlnAsp:
SubjectSite(s)Affected
Cleave:
SubjectSite(s)Affected
RemoveN-Signal:
SubjectSite(s)Affected
RemoveN-Met:
SubjectSite(s)Affected
BreakCys-CysBond:
SubjectSite(s)Affected

FIGURE 3

FIGURE 4

bcl-xL / bcl / bcl-xS / ced-9 / Bax / Blk / Bak / p21 / NGFI-B / N10 / Nak1 / Nur77 / Nurr1 / Nor-1 / Not-1 / RXR / galectin-1 / N-glycan / CNTF / lck / fyn / ZAP-70 / raf / ras / MAP / protein kinase C / PKC / phosphatase calcineurin / NF-AT / AP1 / 14-3-3 / Raf-1 / Bcl-2 / interleukin / IL-1 / IL-3 / cytokine / IGF-1 / CD95 / Apo-1 / RIP / FAF1 / FADD / FAP-1 / TNFR / TRAF / TRAP1 / TRAP2 / TRADD / HIAP1 / HIAP2 / CD40 / CD30 / XIAP / CD2 / CD3 / TCR / Bcl-w / Mcl-1 / NR-13 / BHRF1 / BMWS-HL / E1B19K / Nbk / Mch2 / CPP32 / ICE / FLICE / Nedd-2 / TX / Mch3 / Mch4 / ICH-1s / nuc-1 / DNAseI / caspase / MACH1 / Mch5 / apopain / Yama / ICH / CMH / ced-3 / ced-4 / ced-9 / p53 / MKK3 / MKK1 / MKK2 / MKK4 / BAG-1 / Src / FAST / p38 / p42 / ERK1 / p44 / ERK2 / SAPK / JNK / MEK / C-JUN / MEF2D / ATF2 / calcineurin / ELK-1 / protein phosphatase 2A / raf-1 / IL-1 beta / TNF / PTK / Apaf / p35 / ETS / C-Myc / IL-2 / IL-2 receptor / NF-kappa B / TNFR-1 / TRAIL / Apo-2L / DR4 / death receptor / DR3 / DR2 / DR5 / DR1 / bad / BMPR / BMP-x / TGF / grim / hid / FAN / perforin / Fas-L / Fas / DcR1 / decoy receptor / wsl-1 / NGF receptor / growth factor / RAR

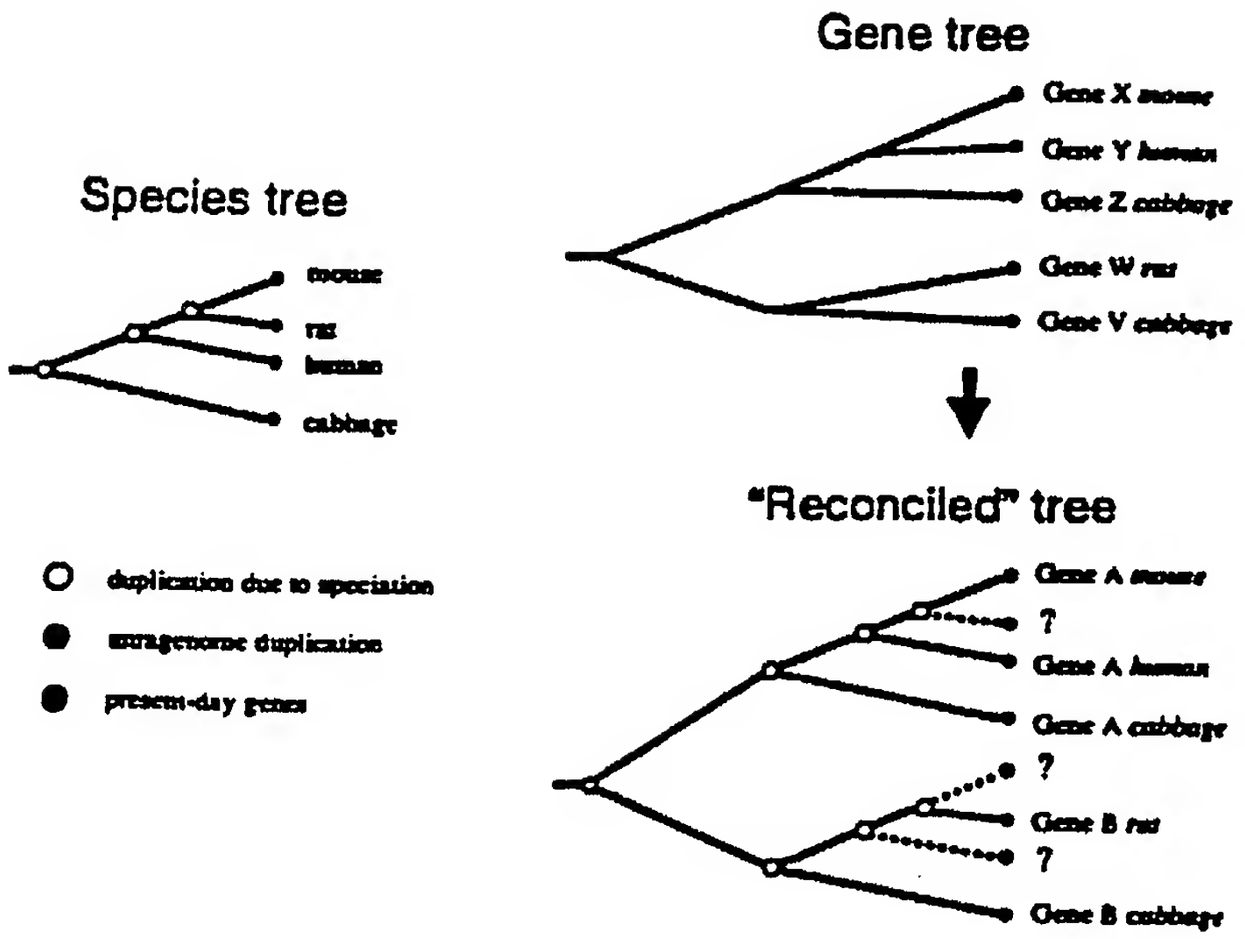

Gene tree
Gene X mouse
Gene Y human
Gene Z cabbage
Gene W rat
Gene V cabbage
Species tree
mouse
rat
human
cabbage
duplication due to speciation
arrangement duplication
present-day genes
"Reconciled" tree
Gene A mouse
?
Gene A human
Gene A cabbage
?
Gene B rat
?
Gene B cabbage

FIGURE 5

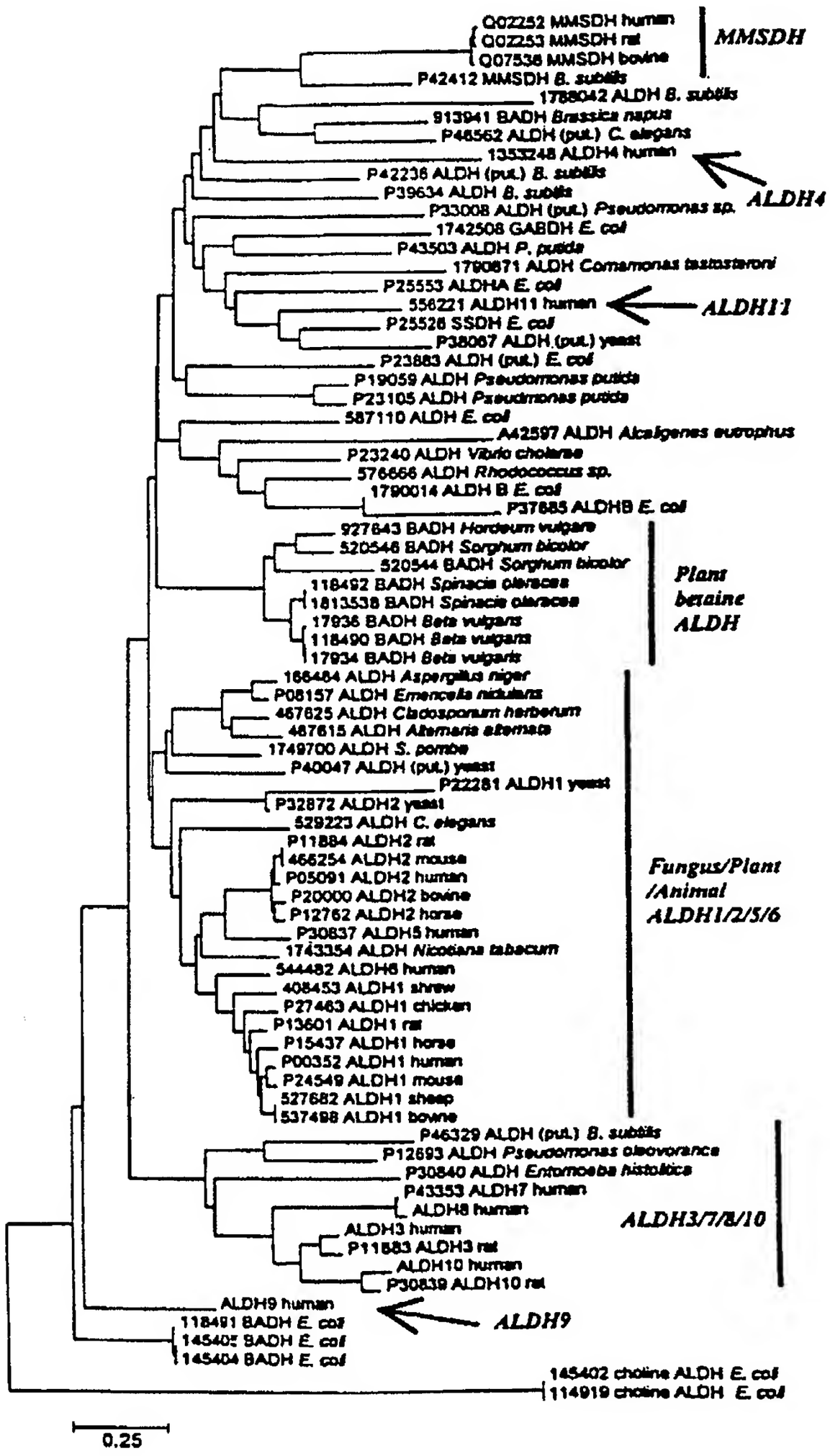

Q02252 MMSDH human
Q02253 MMSDH rat
Q07536 MMSDH bovine
MMSDH
P42412 MMSDH B. subtilis
1788042 ALDH B. subtilis
913941 BADH Brassica napus
P46562 ALDH (put.) C. elegans
1353248 ALDH4 human
P42238 ALDH (put.) B. subtilis
P39634 ALDH B. subtilis
ALDH4
P33008 ALDH (put.) Pseudomonas sp.
1742508 GABDH E. coli
P43503 ALDH P. putida
1790871 ALDH Comamonas testosteroni
P25553 ALDHA E. coli
556221 ALDH11 human
ALDH11
P25526 SSDH E. coli
P38067 ALDH (put.) yeast
P23883 ALDH (put.) E. coli
P19059 ALDH Pseudomonas putida
P23105 ALDH Pseudmonas putida
587110 ALDH E. coli
A42597 ALDH Alcaligenes eutrophus
P23240 ALDH Vibrio cholerae
576666 ALDH Rhodococcus sp.
1790014 ALDH B E. coli
P37685 ALDHB E. coli
927843 BADH Hordeum vulgare
520546 BADH Sorghum bicolor
520544 BADH Sorghum bicolor
118492 BADH Spinacia oleracea
1813538 BADH Spinacia oleracea
17936 BADH Beta vulgaris
118490 BADH Beta vulgaris
17934 BADH Beta vulgaris
Plant betaine ALDH
166484 ALDH Aspergillus niger
P08157 ALDH Emericella nidulans
467625 ALDH Cladosporium herbarum
467615 ALDH Alternaria alternata
1749700 ALDH S. pombe
P40047 ALDH (put.) yeast
P22281 ALDH1 yeast
P32872 ALDH2 yeast
529223 ALDH C. elegans
P11884 ALDH2 rat
466254 ALDH2 mouse
P05091 ALDH2 human
P20000 ALDH2 bovine
P12762 ALDH2 horse
P30837 ALDH5 human
1743354 ALDH Nicotiana tabacum
544482 ALDH6 human
408453 ALDH1 shrew
P27463 ALDH1 chicken
P13601 ALDH1 rat
P15437 ALDH1 horse
P00352 ALDH1 human
P24549 ALDH1 mouse
527682 ALDH1 sheep
537498 ALDH1 bovine
Fungus/Plant /Animal ALDH1/2/5/6
P46329 ALDH (put.) B. subtilis
P12693 ALDH Pseudomonas oleovorance
P30840 ALDH Entamoeba histolitica
P43353 ALDH7 human
ALDH8 human
ALDH3 human
P11883 ALDH3 rat
ALDH10 human
P30839 ALDH10 rat
ALDH3/7/8/10
ALDH9 human
118491 BADH E. coli
145405 BADH E. coli
145404 BADH E. coli
ALDH9
145402 choline ALDH E. coli
114919 choline ALDH E. coli
0.25

FIGURE 6

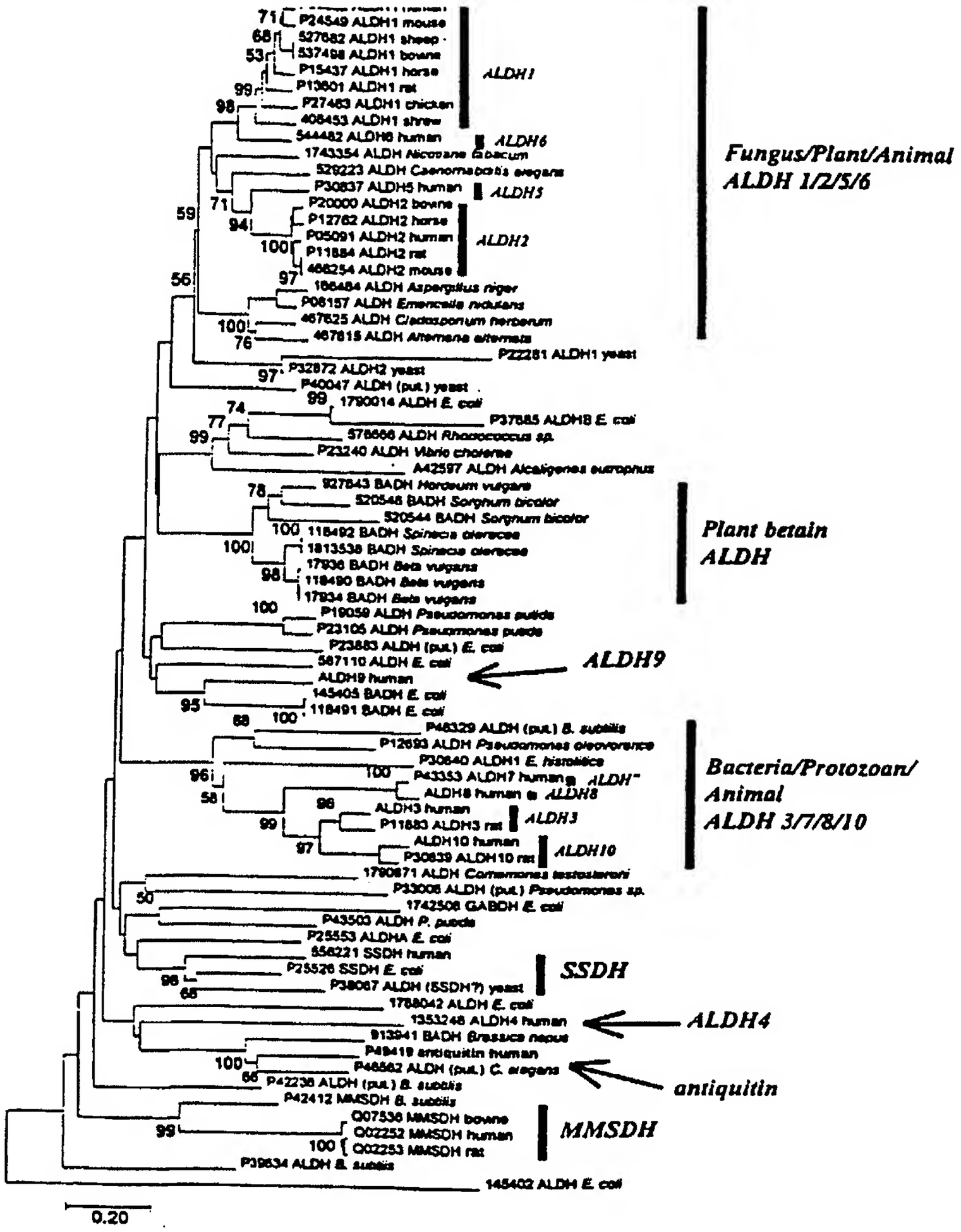
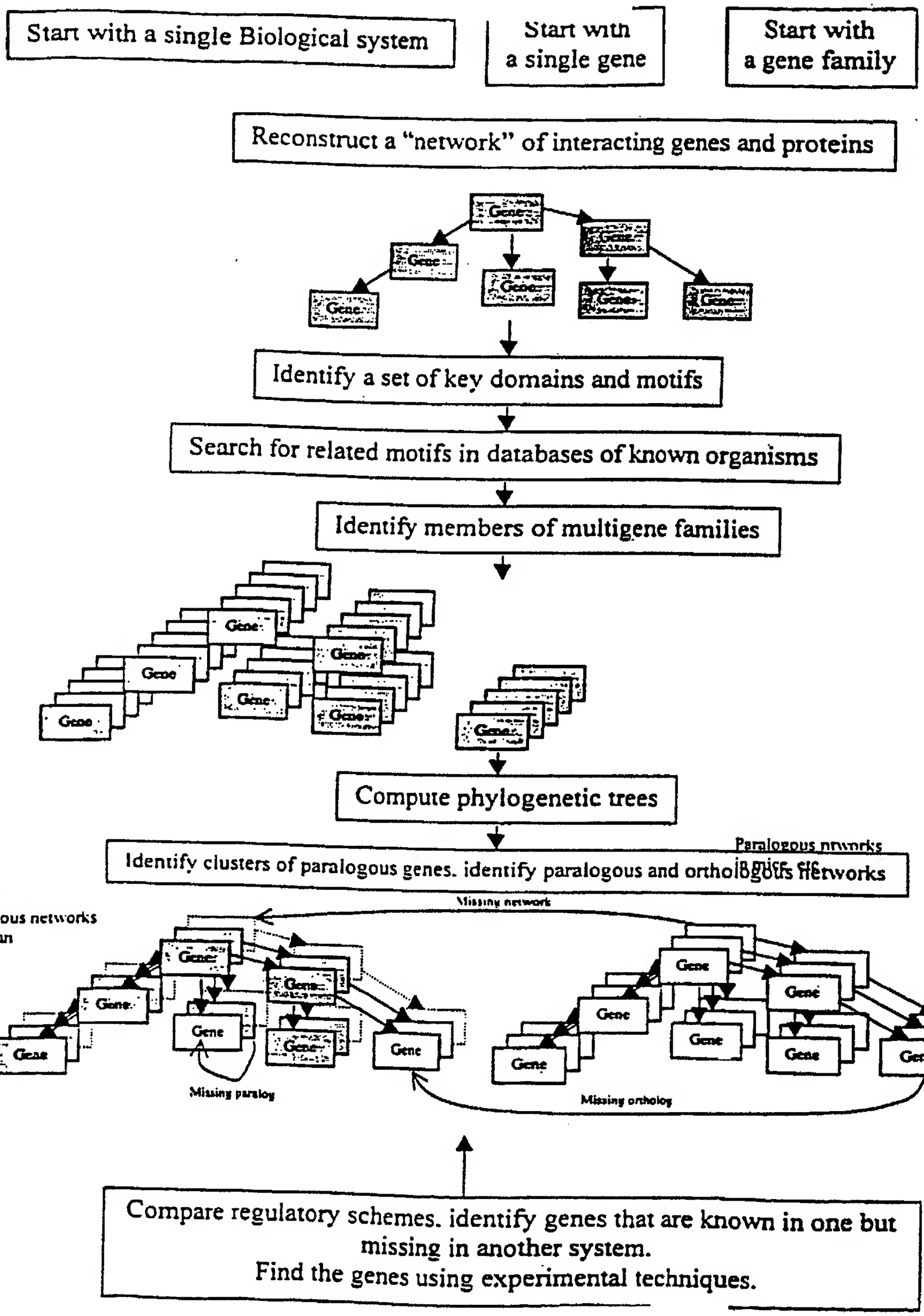

P24549 ALDH1 mouse
527682 ALDH1 sheep
537498 ALDH1 bovine
P15437 ALDH1 horse
P13601 ALDH1 rat
P27463 ALDH1 chicken
406453 ALDH1 shrew
544482 ALDH6 human
ALDH1
ALDH6
1743354 ALDH Nicotiana glauca
529223 ALDH Caenorhabditis elegans
P30837 ALDH5 human
ALDH5
P20000 ALDH2 bovine
P12762 ALDH2 horse
P05091 ALDH2 human
P11884 ALDH2 rat
466254 ALDH2 mouse
ALDH2
166484 ALDH Aspergillus niger
P06157 ALDH Emericella nidulans
467625 ALDH Cladosporium herbarum
467615 ALDH Alternaria alternata
PZ2281 ALDH1 yeast
P32872 ALDH2 yeast
P40047 ALDH (put.) yeast
Fungus/Plant/Animal
ALDH 1/2/5/6
1790014 ALDH E. coli
P37685 ALDH8 E. coli
576666 ALDH Rhodococcus sp.
P23240 ALDH Vibrio cholerae
A42597 ALDH Alcaligenes eutrophus
927643 BADH Hordeum vulgare
520546 BADH Sorghum bicolor
520544 BADH Sorghum bicolor
118492 BADH Spinacia oleracea
1813538 BADH Spinacia oleracea
17936 BADH Beta vulgaris
118490 BADH Beta vulgaris
17934 BADH Beta vulgaris
Plant betain
ALDH
P19059 ALDH Pseudomonas putida
P23105 ALDH Pseudomonas putida
P23883 ALDH (put.) E. coli
587110 ALDH E. coli
ALDH9 human
ALDH9
145405 BADH E. coli
118491 BADH E. coli
P46329 ALDH (put.) B. subtilis
P12693 ALDH Pseudomonas oleovorans
P30840 ALDH1 E. histolitica
P43353 ALDH7 human
ALDH8 human
ALDH*
ALDH8
ALDH3 human
P11883 ALDH3 rat
ALDH3
ALDH10 human
P30839 ALDH10 rat
ALDH10
Bacteria/Protozoan/
Animal
ALDH 3/7/8/10
1790871 ALDH Comamonas testosteroni
P33006 ALDH (put.) Pseudomonas sp.
1742508 GABDH E. coli
P43503 ALDH P. putida
P25553 ALDHA E. coli
556221 SSDH human
P25526 SSDH E. coli
P38067 ALDH (SSDH?) yeast
SSDH
1768042 ALDH E. coli
1353248 ALDH4 human
ALDH4
913941 BADH Brassica napus
P49419 antiquitin human
P46562 ALDH (put.) C. elegans
P42238 ALDH (put.) B. subtilis
antiquitin
P42412 MMSDH B. subtilis
Q07536 MMSDH bovine
Q02252 MMSDH human
Q02253 MMSDH rat
MMSDH
P39634 ALDH B. subtilis
145402 ALDH E. coli
0.20

FIGURE 7

FIGURE 8


Start with a single Biological system
Start with a single gene
Start with a gene family
Reconstruct a "network" of interacting genes and proteins
Gene
Identify a set of key domains and motifs
Search for related motifs in databases of known organisms
Identify members of multigene families
Compute phylogenetic trees
Identify clusters of paralogous genes. identify paralogous and orthologous networks
Paralogous networks
Missing network
Paralogous networks in human
Missing paralog
Missing ortholog
Compare regulatory schemes. identify genes that are known in one but missing in another system.
Find the genes using experimental techniques.

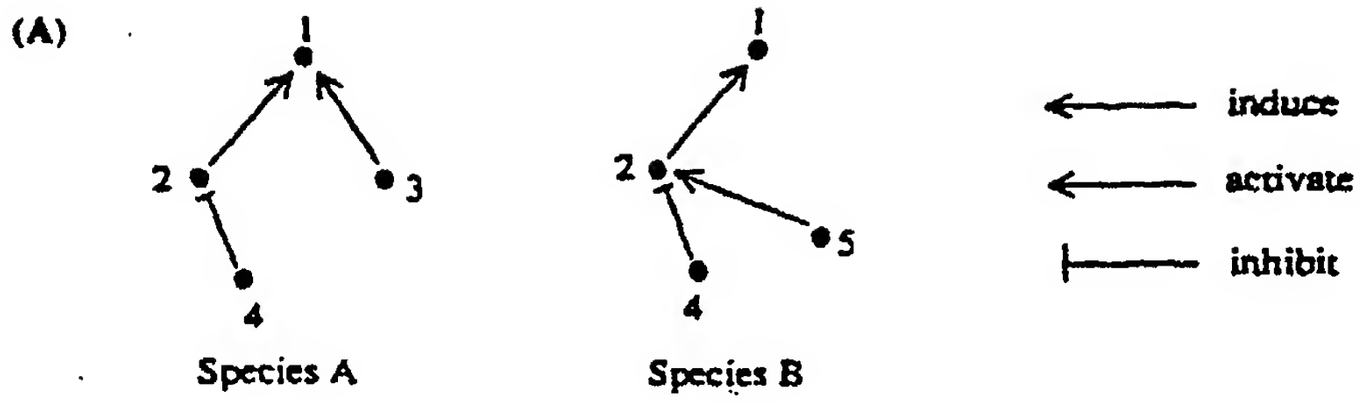

(A)
1
2
3
4
Species A
1
2
5
4
Species B
induce
activate
inhibit
(B)
1
2
3
5
4
A .or. B
(C)
1
2
4
A .and. B
(D)
1
2
3
5
A .xor. B

FIGURE 9

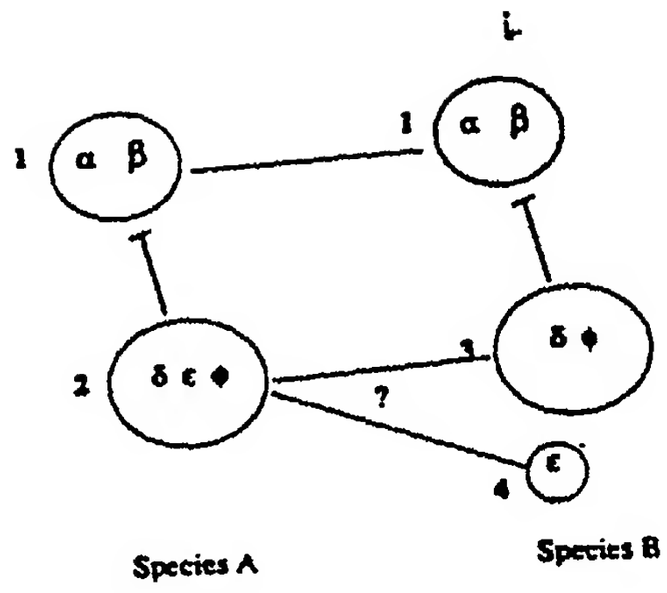


FIGURE 10

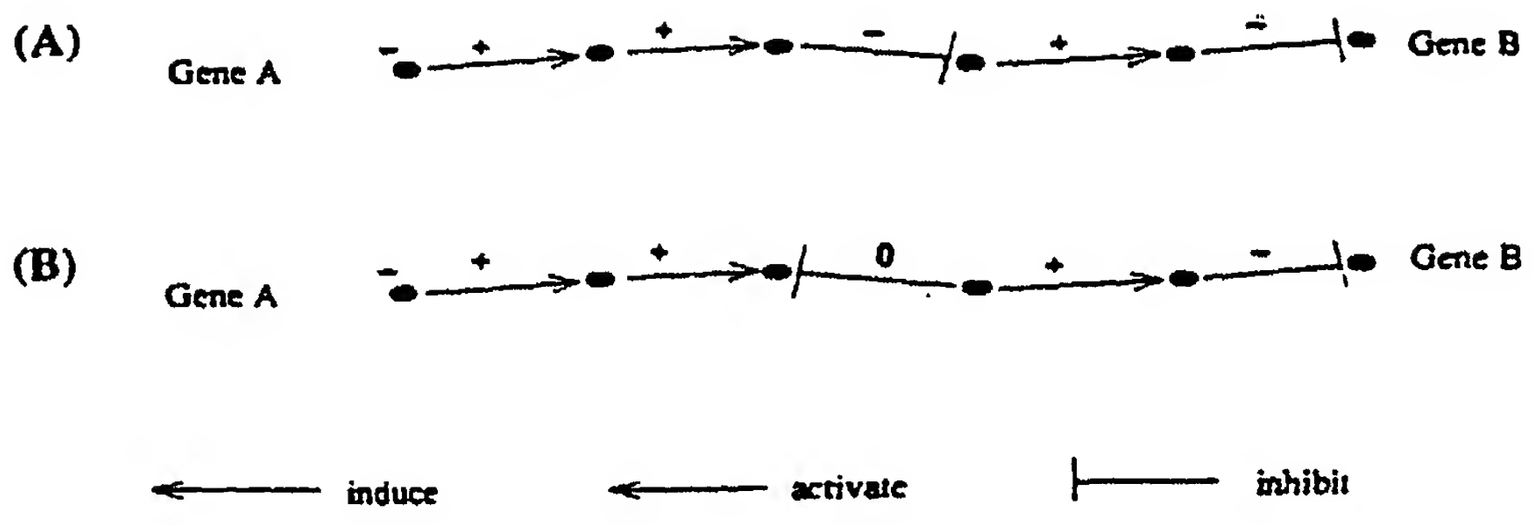


FIGURE 11

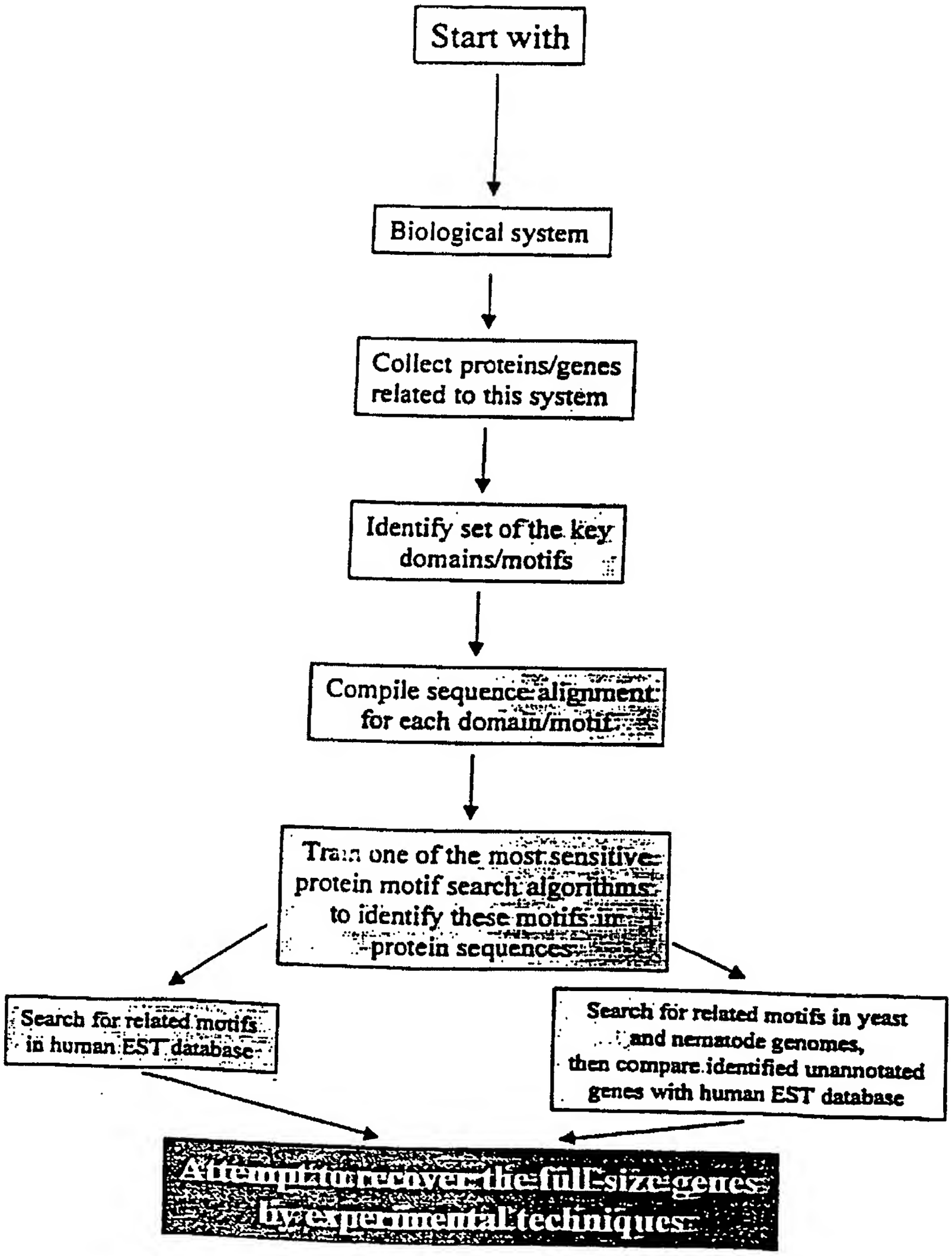

Start with
Biological system
Collect proteins/genes related to this system
Identify set of the key domains/motifs
Compile sequence alignment for each domain/motif
Train one of the most sensitive protein motif search algorithms to identify these motifs in protein sequences
Search for related motifs in human EST database
Search for related motifs in yeast and nematode genomes, then compare identified unannotated genes with human EST database
Attempt to recover the full-size genes by experimental techniques

FIGURE 12

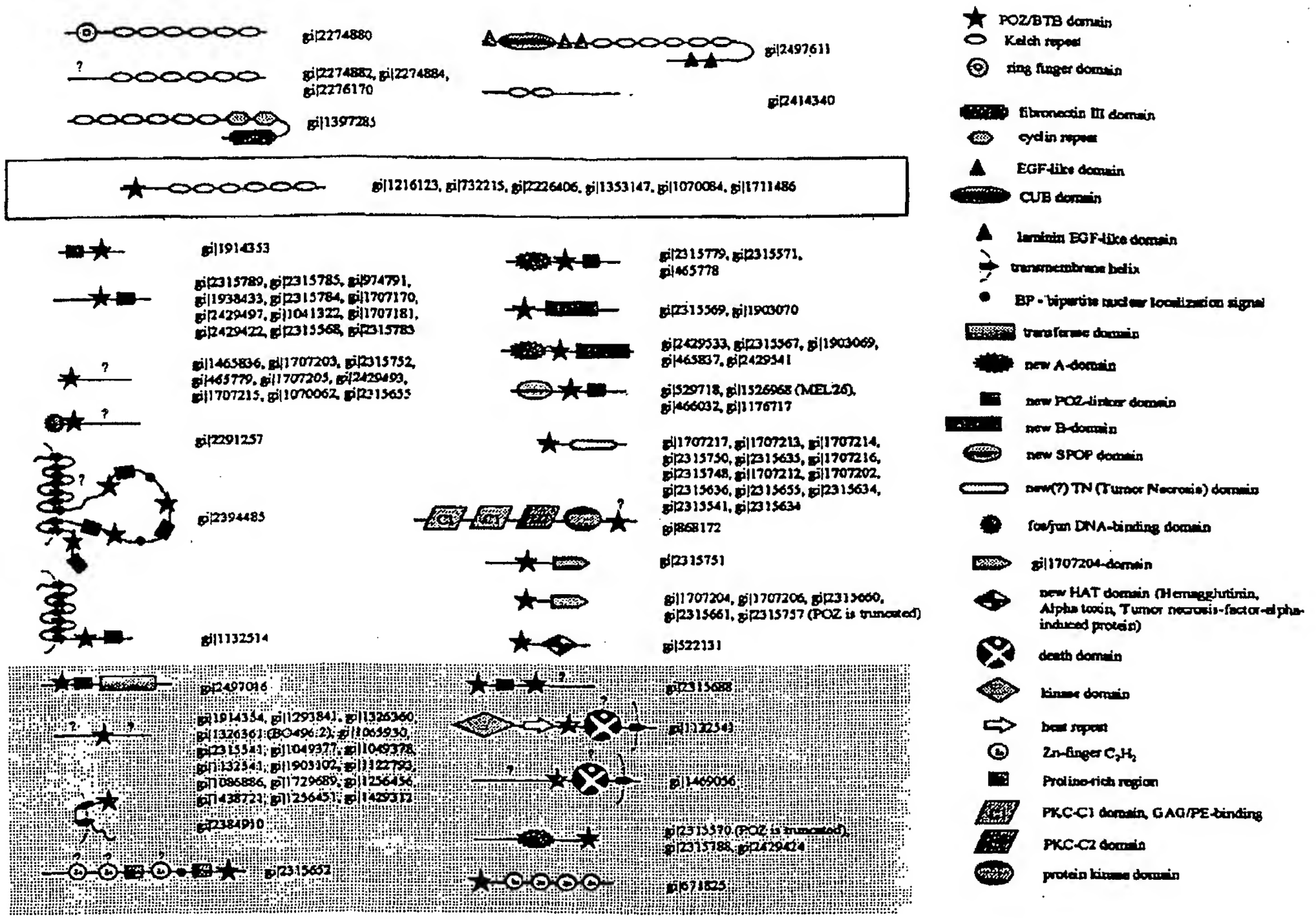

gi|2274880
gi|2274882, gi|2274884, gi|2276170
gi|1397285
gi|2497611
gi|2414340
gi|1216123, gi|732215, gi|2226406, gi|1353147, gi|1070084, gi|1711486
gi|1914353
gi|2315789, gi|2315785, gi|974791, gi|1938433, gi|2315784, gi|1707170, gi|2429497, gi|1041322, gi|1707181, gi|2429422, gi|2315568, gi|2315783
gi|1465836, gi|1707203, gi|2315752, gi|465779, gi|1707205, gi|2429493, gi|1707215, gi|1070062, gi|2315655
gi|2291257
gi|2394485
gi|1132514
gi|2315779, gi|2315571, gi|465778
gi|2315569, gi|1903070
gi|2429533, gi|2315567, gi|1903069, gi|465837, gi|2429541
gi|529718, gi|1526968 (MEL26), gi|466032, gi|1176717
gi|1707217, gi|1707213, gi|1707214, gi|2315750, gi|2315635, gi|1707216, gi|2315748, gi|1707212, gi|1707202, gi|2315636, gi|2315655, gi|2315634, gi|2315541, gi|2315634
gi|868172
gi|2315751
gi|1707204, gi|1707206, gi|2315660, gi|2315661, gi|2315757 (POZ is truncated)
gi|522131
gi|2497016
gi|1914354, gi|1293841, gi|1326360, gi|1326361 (BC496.2), gi|1065930, gi|2315541, gi|1049377, gi|1049378, gi|132541, gi|1903102, gi|1322793, gi|1086886, gi|1729689, gi|1256456, gi|1438721, gi|1256451, gi|1429312
gi|2384910
gi|2315652
gi|2315688
gi|132543
gi|1469056
gi|2315590 (POZ is truncated), gi|2315788, gi|2429424
gi|671825
POZ/BTB domain
Kelch repeat
ring finger domain
fibronectin III domain
cyclin repeat
EGF-like domain
CUB domain
laminin EGF-like domain
transmembrane helix
BP - bipartite nuclear localization signal
transferase domain
new A-domain
new POZ-linker domain
new B-domain
new SPOP domain
new(?) TN (Tumor Necrosis) domain
fos/jun DNA-binding domain
gi|1707204-domain
new HAT domain (Hemagglutinin, Alpha toxin, Tumor necrosis-factor-alpha-induced protein)
death domain
kinase domain
beat repeat
Zn-finger C_2H_2
Proline-rich region
PKC-C1 domain, GAG/PE-binding
PKC-C2 domain
protein kinase domain

Figure 13

>gi|2210766|gb|AA481214|AA481214 aa34e02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815162 5' similar to WP:W07A12.4 CE03795 ;, mRNA sequence [Homo sapiens]
CATGGCTTCCTGGACACCAACCCTGCCATCCGGGAGCAGACGGTCAAGTCCATGCTGCTCCTGGCCCCAA
AGCTGAACGAGGCCAACCTCAATGTGGAGCTGATGAAGCACTTTGCACGGCTACAGGCCAAGGATGAACA
GGGCCCCATCCGCTGCAACACCACAGTCTGCCTGGGCAAAATCGGCTCCTACCTCAGTGCTAGCACCAGA
CACAGGGTCCTTACCTCTGCCTTCAGCCGAGCCACTAGGGACCCGTTTGCACCGTCCCGGGTTGCGGGTG
TCCTGGGCTTTGCTGCCACCCACAACCTCTACTCAATGAACGACTGTGCCCAGAAGATCCTGCCTGTGCT
CTGCGGTCTCACTGTAGATCCTGAGAAATCCGTGCGAGACCAGGCCTTCAAGGCA

>gi|1349211|gb|W51957|W51957 zc45f01.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325273 5', mRNA sequence [Homo sapiens]
CCTTCGAGTTCGGCAATGCTGGGGCCGTTGTCCTCACGCCCCTCTTCAAGGTGGGCAAGTTCCTGAGCGC
TGAGGAGTATCAGCAGAAGATCATCCCTGTGGTGGTCAAGATGTTCTCATCCACTGACCGGGCCATGCGC
ATCCGNCTCCTGCAGCAGATGGAGCAGTTCATCCAGTACCTTGACGAGCCAACAGTCAACACCCAGATCT
TCCCCCACGTCGTACATGGCTTCCTGGACACCAACCCTGCCATCCGGGAGCAGACGGTCAAGTCCATGCT
GCTCCTGGCCCCAAAGCTGAACGAGGCCAACCTCAATGTGGAGCTGATGAAGCACTTTGCACGGCTACAG
GCCAAGGATGAACAGGGCCCCATCCGCTGCAACACCACAGTCTGCCTGGGCAAAATCGGCTCCTACCTCA
GTGCTAGCACCAGACACAGGGTCCTTACCTCTG

Figure 14A

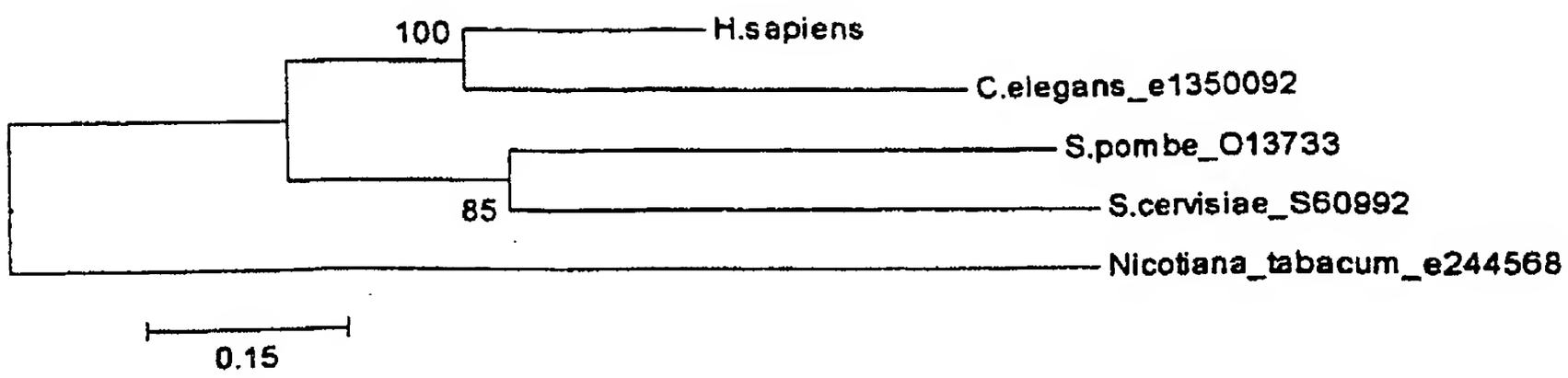

100
H.sapiens
C.elegans_e1350092
S.pombe_O13733
85
S.cervisiae_S60992
Nicotiana_tabacum_e244568
0.15

Figure 14B

```
BASE COUNT       405 a      545 c      493 g      278 t        6 others
ORIGIN
        1 cagccgaagc amgcaaaaat tcttccagga gctgagcaag agcctggacg cattccctga
       61 ggayttctgt cggcacaagg tgctgcccca gctgctgacc gccttcgagt tcggcaatgc
      121 tggggccgtt gtcctcacgc ccctcttcaa ggtgggcaag ttcctgagcg ctgaggagta
      181 tcagcagaag atcatccctg tggtggtcaa gatgttctca tccactgacc gggccatgcg
      241 catccgcctc ctgcagcaga tggagcagtt catccagtac cttgacgagc caacagtcaa
      301 cacccagatc ttcccccacg tcgtacatgg cttcctggac accaaccctg ccatccggga
      361 gcagacggtc aagtccatgc tgctcctggc cccaaagctg aacgaggcca acctcaatgt
      421 ggagctgatg aagcactttg cacggctaca ggccaaggat gaacagggcc ccatccgctg
      481 caacaccaca gtctgcctgg gcaaaatcgg ctcctacctc agtgctagca ccagacacag
      541 ggtccttacc tctgccttca gccgagccac tagggacccg tttgcaccgt cccgggttgc
      601 gggtgtcctg ggctttgctg ccacccacaa cctctactca atgaacgact gtgcccagaa
      661 gatcctgcct gtgctctgcg gtctcactgt agatcctgag aaatccgtgc gagaccaggc
      721 cttcaaggcm wttcggagct tcctgtccaa attggagtct gtgtcggagg acccgaccca
      781 gctggaggaa gtggagaagg atgtccatgc agcctccagc cctggcatgg gaggagccgc
      841 agctagctgg gcaggctggg cgtgaccggg gtctcctcac tcacctccaa gctgatccgt
      901 tcgcacccaa ccactgcccc aacagaaacc aacattcccc aaagacccac gcctgaagga
      961 gttcctgccc cagcccccac ccctgttcct gccaccccta caacctcagg ccactgggag
     1021 acgcaggagg aggacaagga cacagcagag gacagcagca ctgctgacag atgggacgac
     1081 gaagactggg gcagcctgga gcaggaggcc gagtctgtgc tggcccagca ggacgactgg
     1141 agcaccgggg gccaagtgag ccgtgctagt caggtcagca actccgacca caaatcctcc
     1201 aaatccccag agtccgactg gagcagctgg gaarctgagg gctcctggga acagggctgg
     1261 caggagccaa gctcccagga gccacctyct gacggtacac ggctggccag cgagtataac
     1321 tggggtggcc cagagtccag cgacaagggc gacccccttcg ctaccctgtc tgcacgtccc
     1381 agcacccagc cgaggccaga ctcttggggt gaggacaact gggagggcct cgagactgac
     1441 agtcgacagg tcaaggctga gctggcccgg aagaagcgcg aggagcggcg gcgggagatg
     1501 gaggccaaac gcgccgagag gaaggtgcca agggccccat gaagctggga gcccggaagc
     1561 tggactgaac cgtggcggtg gcccttcccg gctgcggaga gcccgcccca cagatgtatt
     1621 tattgtacaa accatgtgag cccggccgcc cagccaggcc atctcacgtg tacataatca
     1681 gagccacaat aaattctatt tcacaaaaaa aaaaaaaaaa aaaaaaa
//
```

Figure 14C

```
                  5        10        15        20        25        30
  1  S R S X Q K F F Q E L S K S L D A F P E D F C R H K V L P Q
 31  L L T A F E F G N A G A V V L T P L F K V G K F L S A E E Y
 61  Q Q K I I P V V V K M F S S T D R A M R I R L L Q Q M E Q F
 91  I Q Y L D E P T V N T Q I F P H V V H G F L D T N P A I R E
121  Q T V K S M L L L A P K L N E A N L N V E L M K H F A R L Q
151  A K D E Q G P I R C N T T V C L G K I G S Y L S A S T R H R
181  V L T S A F S R A T R D P F A P S R V A G V L G F A A T H N
211  L Y S M N D C A Q K I L P V L C G L T V D P E K S V R D Q A
241  F K A X R S F L S K L E S V S E D P T Q L E E V E K D V H A
271  A S S P G M G G A A A S W A G W A
```

Figure 14D

>sp|P15533|RPT1_MOUSE DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR (J03776) rpt-1r [Mus musculus] Length = 353

Score = 92.0 bits (237), Expect = 6e-20

```
Query 194 VMELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILEGSVRNSMWRPAPFKCPTCRK 373
          V+E+++E++TCPIC  L  +P    C+H+FC+ C+    E S RN+         CP CR
Sbjct 5   VLEMIKEEVTCPICLELLKEPVSADCNHSFCRACITLNYE-SNRNT---DGKGNCPVCRV 60

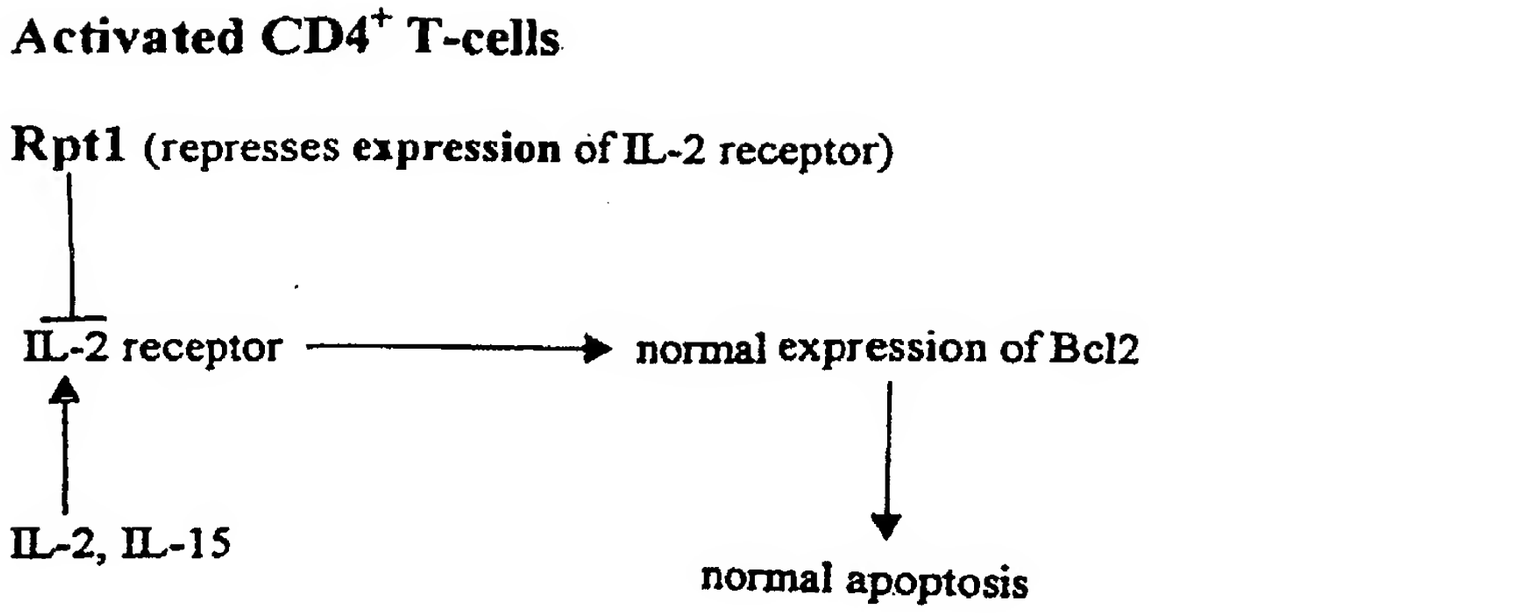
Query 374 ETSATGINSLQVNYSLKGIVEKYNKIKISP----KMPVCKGHMGQPLNIFCLTDMQLICG 541
                +L+ N  +  IVE+    K  P    K+ +C  H G+ L +FC   DM +IC
Sbjct 61  PYP---FGNLRPNLHVANIVERLKGFKSIPEEEQKVNICAQH-GEKLRLFCRKDMMVICW 116

Query 542 ICATRGEHTKHVFCSIEDAYAQERDAFESLFQSF--------ETWRRGDALSRLDTMETSK 700
          +C    EH  H    IE+   + ++  +               + W+    L R+D
Sbjct 117 LCERSQEHRGHQTALIEEVDQEYKEKLQGALWKLMKKAKICDEWQDDLQLQRVDW------ 171

Query 701 RKSLQLMTKDSDKVKEFFEKLQHTLDQKKNEILSDFETMKLAVMQAYDPEINKL 862
             +Q+   + + V+  F+ L+  LD K+NE L   +  K  VM+  +   N+L
Sbjct 172 ENQIQI---NVENVQRQFKGLRDLLDSKENEELQKLKKEKKEVMEKLEESENEL 222
```

Homology covers ring finger, B-box and the beginning of coiled coil domain in the CLL ring finger protein

Figure 15


Activated CD4+ T-cells
Rpt1 (represses expression of IL-2 receptor)
IL-2 receptor
normal expression of Bcl2
IL-2, IL-15
normal apoptosis

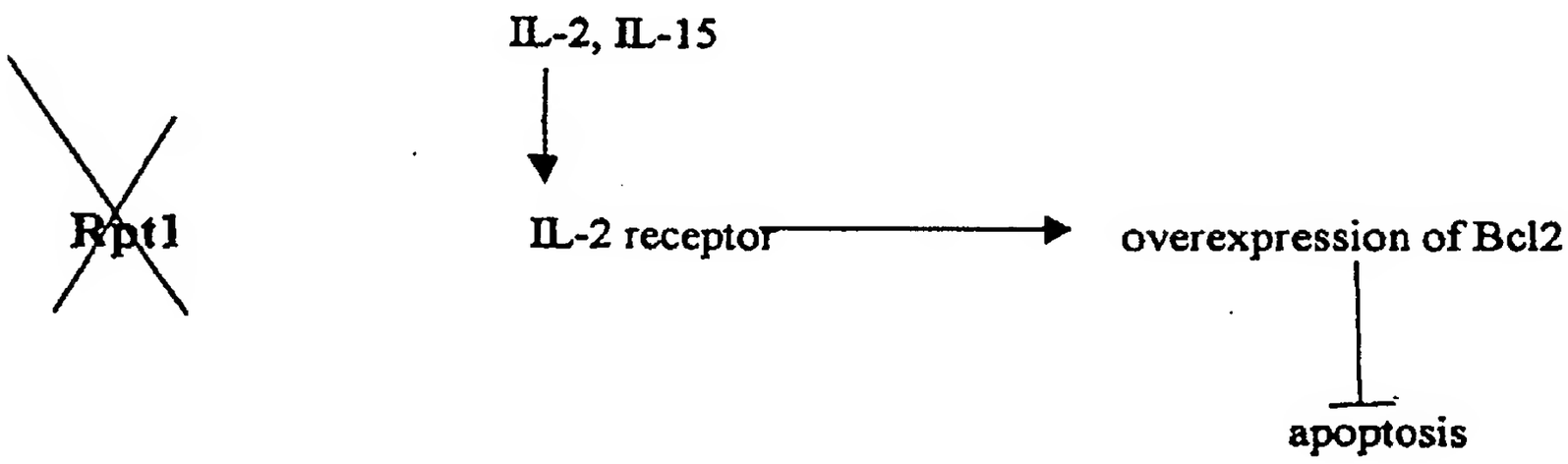

When rpt1 is knocked out:
IL-2, IL-15
Rpt1
IL-2 receptor
overexpression of Bcl2
apoptosis

Figure 16

```
TBLASTN 2.0.8 [Jan-05-1999]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= gi|2137498|Mad3m
         (205 letters)


gb|AA278224|AA278224 zs77e05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703520 5'
           similar to TR:G1184157 G1184157 MAX-INTERACTING
           TRANSCRIPTIONAL REPRESSOR. ;
           Length = 430

 Score =  209 bits (526), Expect = 1e-53
 Identities = 104/124 (83%), Positives = 116/124 (92%), Gaps = 1/124 (0%)
 Frame = +2

Query: 1   MEPVASNIQVLLQAAEFLERREREAEHGYASLCPHHSPGTVCRRRKPPLQAPGALNSGRS 60
           MEP+ASNIQVLLQAAEFLERREREAEHGYASLCPH SPG + RR+K P QAPGA +SGRS
Sbjct: 56  MEPLASNIQVLLQAAEFLERREREAEHGYASLCPHRSPGPIHRRKKRPPQAPGAQDSGRS 235

Query: 61  VHNELEKRRRAQLKRCLEQLRQQMPLGVDCTRYTTLSLL-RARVHIQKLEEQEQQARRLK 119
           VHNELEKRRRAQLKRCLE+L+QQMPLG DC RYTTLSLL RAR+HIQKLE+QEQ+AR+LK
Sbjct: 236 VHNELEKRRRAQLKRCLERLKQQMPLGGDCARYTTLSLLRRARMHIQKLEDQEQRARQLK 415

Query: 120 EKLRS 124
           E+LR+
Sbjct: 416 ERLRT 430


dbj|C02407|C02407 HUMGS0012279, Human Gene Signature, 3'-directed cDNA sequence.
           Length = 348

 Score = 97.5 bits (239), Expect = 6e-20
 Identities = 51/63 (80%), Positives = 56/63 (87%)
 Frame = +3

Query: 125 KQQSLQQQLEQLQGLPGARERERLRADSLDSSGLSSERSDSDQEDLEVDVENLVFGTETE 184
           KQQSLQ+   QL+GL GA ERERLRADSLDSSGLSSERSDSDQE+LEVDVE+LVFG E E
Sbjct: 45  KQQSLQRXWMQLRGLAGAAERERLRADSLDSSGLSSERSDSDQEELEVDVESLVFGGEAE 224

Query: 185 LLQ 187
           LL+
Sbjct: 225 LLR 233
```

Figure 17A

```
BASE COUNT       130 a    234 c    258 g    106 t      5 others
ORIGIN
        1 cagccgcttg ctccggccgg caccctaggc cgcagtccgc caggctgtcg ccgacatgga
       61 acccttggcc agcaacatcc aggtcctgct gcaggcggcc gagttcctgg agcgccgtga
      121 gagagaggcc gagcatggtt atgcgtccct gtgcccgcat cgcagtccag gccccatcca
      181 caggaggaag aagcgacccc cccaggctcc tggcgcgcag gacagcgggc ggtcagtgca
      241 caatgaactg gagaagcgca ggagggccca gttgaagcgg tgcctggagc ggctgaagca
      301 gcagatgccc ctgggcggcg actgtgcccg gtacaccacg ctgagcctgc tgcgccgtgc
      361 caggatgcac atccagaagc tggaggatca ggagcagcgg gcccgacagc tcaaggagag
      421 gctgcgcaca aagcagcaga gcctgcagcg gcantggatg cagctccggg ggctggcagg
      481 ngcggccgag cgggagcgnc tgcgggcgga cagtctggac tcctcaggcc tctcctctga
      541 gcgctcagac tcagaccaag aggagctgga ggtggatgtg gagagcctgg tgtttggggg
      601 tgaggccgag ctgctgcggg gcttcgtcgc cggccaggag cacagctact cgcacgtcgg
      661 cggcgcctgg ctatgatgtt cctcacccan ggcgggcctc tgccctctta ctcgttgccc
      721 aagcccactt tnc
```

Figure 17B

C

>*Mad*3h(Putative)
MEPLASNIQVLLQAAEFLERREREAEHGYASLCPHRSPGPIHRRKKRPPQAPGAQDSGRSVHNELEKRRRAQLK
RCLERLKQQMPLGGDCARYTTLSLLRRARMHIQKLEDQEQRARQLKERLRTKQQSLQRXWMQLRGLAGAAERER
LRADSLDSSGLSSERSDSDQEELEVDVESLVFGGEAELLRGFVAGQEHSYSHVGGAWL

D

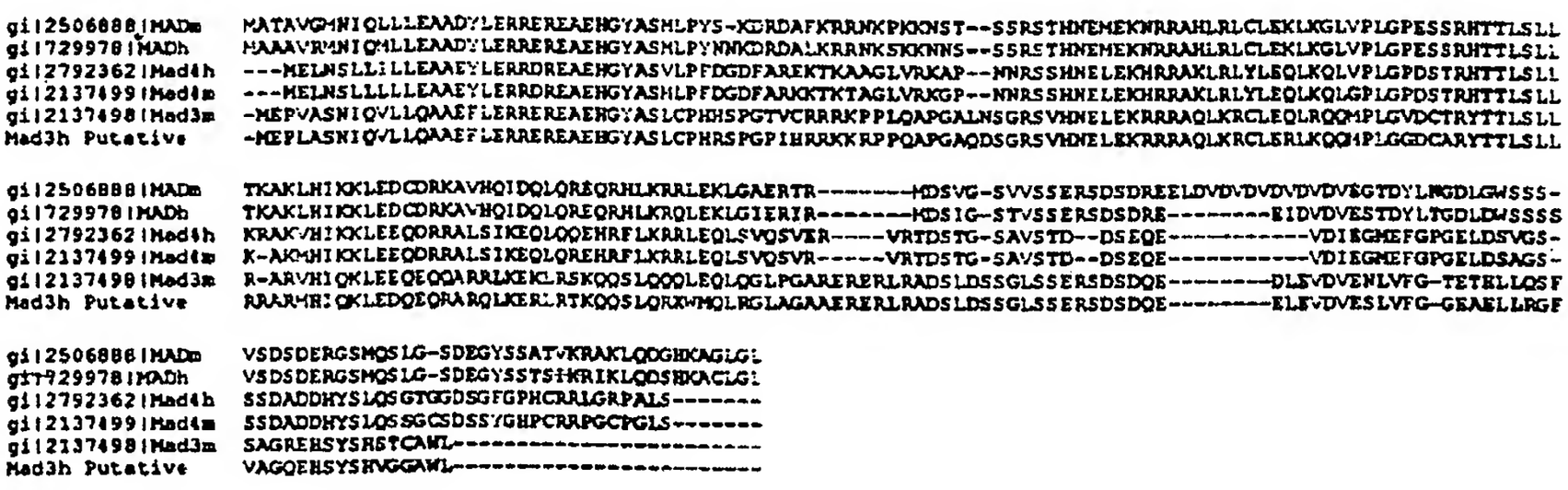
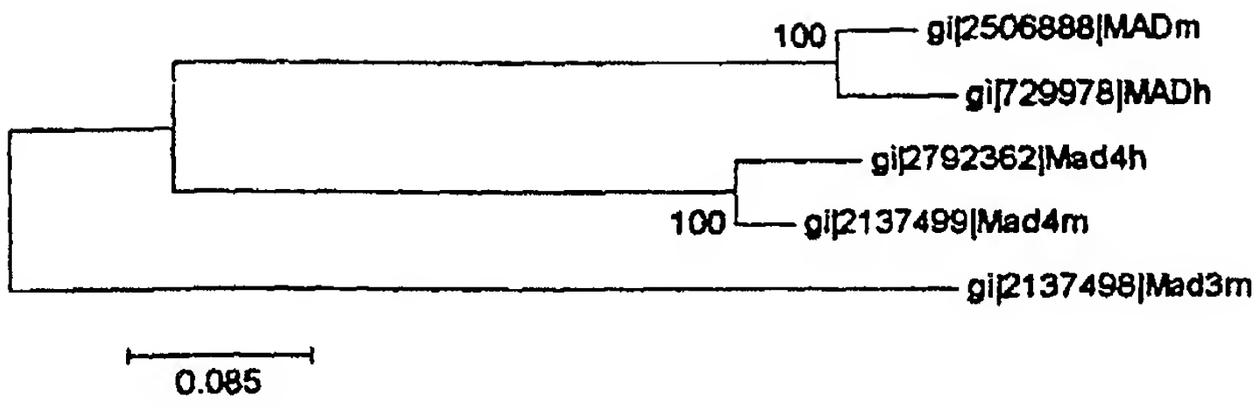


Figure 17 C-D

A.



B.

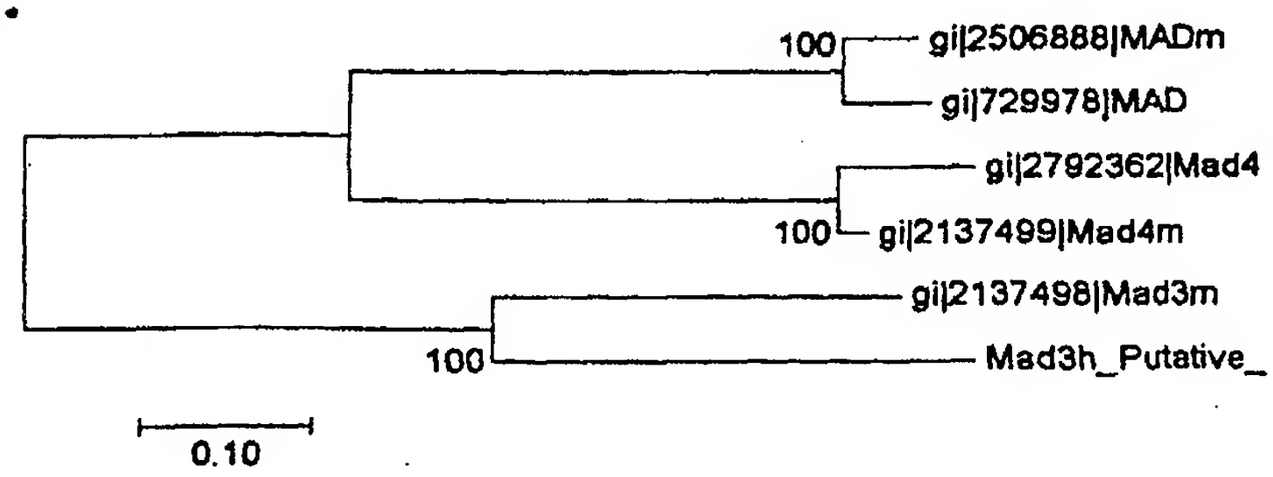


Figure 18. A-B

```
% lexsemsub.pl
% lexsemsub.pat
% revised  March 17, 2000
%            LEXICON OF SUBSTANCES AND STRUCTURES
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
:-multifile(phrase/5).
:-multifile(wdef/3).
:-unknown(_,fail).
phrase('[',protein, ['[',gamma,']','-',aminobutyric, acid, a], 'GA
BAA', r).  % ?
phrase('[',smallmolecule, ['[',zeta,']',1, subunit], '[zeta]1 subu
nit', r).  % ?
phrase(116, protein,[116,'-',kd,fyn,'-',associated,protein],'116-k
D Fyn-associated protein',r).
phrase(116, protein,[116,'-',kd,protein], '116-kd protein',r).
phrase(3,protein, [3,'-',kinase,'-',akt],  '3-kinase-Akt',r).
phrase(ability, affirmation, [ability, to], [], r).
phrase(agc,protein, [agc, protein, kinases], 'AGC', r).
phrase(akt,protein, [akt, mutant], 'Akt mutant', r).
phrase(alternative,substance,[alternative,ntf],'alternative NTF',r
).
phrase(antibody, protein,[antibody,to,phosphotyrosine],'anti-phosp
hotyrosine',r).
phrase(antigen, complex,[antigen,receptor], 'antigen receptor',r).
phrase(ap, protein, [ap,'-',1],'AP-1',r).
phrase(aspargine,site,[aspargine,'-',141],'aspargine-141',r).
phrase(b, cell, [b,cell], 'B cell', r).
phrase(b, cell, [b,cells], 'B cell', r).
phrase(b, species,[b,lymphoblastoid,cells], 'B lymphoblastoid cell
s',r).
phrase(b,cell,[b,lymphoblastoid,cells], 'B lymphoblastoid cells',r
).
phrase(b7, protein, [b7,'-','1'], 'B7-1',r).
phrase(bcl,protein,[bcl,'-',2],'Bcl-2',r).
phrase(c, protein, [c,'-',jun] , 'c-Jun',r).
phrase(camk, protein, [camk, iv], 'CaMK IV',r).
phrase(casp, protein,[casp,'-',3], 'caspase-3',r).
phrase(caspase,protein,[caspase,'-',3,family,protease], 'caspase-3
 family protease',r).
phrase(caspase,protein,[caspase,'-',3,precursor],'caspase-3 precur
sor',r).
phrase(caspase,protein,[caspase,'-',3],'caspase-3',r).
phrase(caspase,protein,[caspase,-,3],'caspase-3',r).
```

Appendix A

```
phrase(caspase,protein,[caspase,'-',6],'caspase-6',r).
phrase(caspase,protein,[caspase,'-',7],'caspase-7',r).
phrase(catalytic, domain, [catalytic, domain], 'catalytic domain',
r).
phrase(cleavage,site,[cleavage,site],'cleavage site',r).
phrase(cleavage,substance,[cleavage,products],'cleavage products',
r).
phrase(cooh,substance, [cooh,'-',terminal,fragment], 'COOH-termina
l fragment',r).
phrase(crk,protein,[crk,proteins], 'crk proteins',r0.
phrase(crkl, complex,[crkl,'-',c3g,complex],'crkl-c3g complex',r).
phrase(dcp,protein,[dcp,-,1],'DCP-1',r).
phrase(did, negation, [did, not], not, r).
phrase(ebv,species, 'Epstein-Barr virus',r).
phrase(epstein, species, [epstein,'-',barr,virus],'Epstein-Barr vi
rus',r).
phrase(familial,disease,[familial,alzheimer,'''',s,disease],'famil
ial Alzheimer''''s disease',r).
phrase(gene, gene, [gene,encoding,interleukin,'-',2],'gene encodin
g interleukin-2', r).
phrase(gst, protein, [gst,'-','fyn','-',sh2], 'GST-Fyn-SH2',r).
phrase(gst, protein, [gst,'-','fyn','-',sh3], 'GST-Fyn-SH3',r).
phrase(gtp, complex,[gtp,exchange,of,rap1],'GTP exchange of Rap1',
r).
phrase(guanidine, protein, [guanidine,nucleotide,'-',releasing,fac
tor,c3g],'guanidine nucleotide-releasing factor C3G',r).
phrase(guanidine, smallmolecule, [guanidine,nucleotide],'guanidine
 nucleotide',r).
phrase(guanosine, smallmolecule,[guanosine,triphosphate],'guanosin
e triphosphate',r).
phrase(guanosine,smallmolecule,[guanosine,diphosphate],'guanosine
diphosphate',r).
phrase(h4,cell,[h4,cell,line], 'H4 cell line',r).
phrase(h4,cell,[h4,human,neuroglioma,cells], 'H4,human,neuroglioma
,cells',r).
phrase(ha, protein, [ha, '-', '[',delta,']',phpkb],'HA-[Delta]PHPK
B',r).
phrase(hla, protein, [hla,'-',dr7], 'HLA-DR7',r).
phrase(i, protein, [i, '[',kappa, ']',b,'-','[',beta,']'], 'I[ka
ppa]B-[beta]',r).
phrase(i,protein, [i, '[',kappa, ']',b,'-','[',alpha,']'], 'I[kap
pa]B-[alpha]',r).
phrase(i,protein, [i, '[',kappa, ']',b], 'I[kappa]B',r).
```

```
phrase(ice,protein,[ice,'/',ced,'-',3],'ICE/Ced-3',r).
phrase(il, gene, [il,'-',2,gene], 'gene encoding interleukin-2', r
).
phrase(il, protein, [il,'-',2], 'interleukin-2',r).
phrase(in, interm, [in, the, case, of],[], r).
phrase(in,state,[in,the,anergic,state], inactive,r).
phrase(inducible, cell, [inducible,h4,cell], 'inducible H4 cell',r
).
phrase(interleukin, protein, [interleukin,'-',2],r).
phrase(interleukin, protein,[interleukin, '-', 3], 'interleukin-3
',r).
phrase(interleukin,protein,[interleukin,'-',1,beta,converting,enzy
me], 'interleukin-1 beta converting enzyme',r).
phrase(jurkat, cell, [jurkat, cell], 'Jurkat cell', r).
phrase(jurkat, cell, [jurkat, cells], 'Jurkat cell', r).
phrase(kif3a,protein,[kif3a,'/',3,b],'KIF3A/3B',r).
phrase(lbl, cell, [lbl,'-',drf, cells], 'LBL-DR7 cells',r).
phrase(lbl,cell,[lbl,'-',dr7,cells],'LBL-DR7 cells',r).
phrase(let, protein, [let,'-',23], 'Let-23', r).
phrase(may, probability,[may, be], possible, r).
phrase(myc, protein, [myc, '-', p70s6kd3e], 'Myc-p70s6kD3E',r).
phrase(myc, protein, [myc, '-', pdk1], 'Myc-PDK1',r).
phrase(myc,protein,[myc,'-',p70s6k],'Myc-p70s6k',r).
phrase(myc,protein,[myc,'-',p70s6ke389d3e], 'Myc-p70s6kE389D3E',r)
.
phrase(myr, protein,[myr,'-',akt], 'Myr-Akt',r).
phrase(n,protein, [n,'-',methyl,'-',d,'-',aspartate, receptor], 'N
MDAR', r).
phrase(n,protein, [n,'-',methyl,'-',d,'-',aspartate], 'NMDA').
phrase(native, cell, [native,h4,cell],'native H4 cell',r).
phrase(nf, protein, [nf,'-','[',kappa,']',b], 'NF-[kappa]B',r).
phrase(nh2, site, [nh2,'-',terminal], 'NH2-terminal',r).
phrase(nh2,substance,[nh2,'-',terminal,fragment], 'NH2-terminal fr
agment',r).
phrase(nih, cell,[nih,'-',3,t3,fibroblasts], 'NIH-3T3 fibroblasts'
, r).
phrase(nih,cell,[nih,'-','3t3', fibroblasts],'NIH-3T3 fibroblasts'
,r).
phrase(normal,substance,[normal,ntf],'normal NTF',r).
phrase(nuclear, protein, [nuclear, factor, kappa, b],'NF-[kappa]B'
, r).
phrase(p150Glued,protein,[p150Glued,-,arp1],'p150Glued-Arp1',r).
phrase(phosphate,phosphorylate2, [phosphate, incorporated, into],
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phosphorylate,r).

phrase(phosphatidylinositol, smallmolecule,[phosphatidylinositol,1
,',',4,',',5,'-',triphosphate], 'phosphatidylinositol 1,4,5-tripho
sphate',r).
phrase(phosphoinositide, protein, [phosphoinositide,'-',dependent,
 protein, kinase], 'PDK1',r).
phrase(phospholipase, protein, [phospholipase,c,'-',1],'phospholip
ase C-1', r).
phrase(poly,protein,[poly,'(',adp,'-',ribose,')',polymerase],'poly
(ADP-ribose) polymerase',r).
phrase(polyvinylidene, structure,[polyvinylidene, difluoride, memb
ranes],'polyvinylidene difluoride membranes',r).
phrase(presenilin, protein,[presenilin,1],'presenilin 1',r).
phrase(presenilin,protein,[presenilin,2],'presenilin,2',r).
phrase(productively, state,[productively,stimulated],active,r).
phrase(protein, protein, [protein,tyrosine,kinase],'protein tyrosi
ne kinase', r).
phrase(protein,protein,[protein,kinase,c],'protein kinase C',r).
phrase(ps2,substance,[ps2,'-',ctf],'presenilin 2 COOH-terminal fra
gment',r).
phrase(ps2,substance,[ps2,cleavage,fragment], 'presenilin 2 cleava
ge fragment', r).
phrase(pvdf, structure, [pvdf, membranes],'polyvinylidene difluori
de membranes',r).
phrase(raf, protein, [raf,'-',1], 'Raf-1', r).
phrase(raf,protein,[raf,'-',1], 'Raf-1',r).
phrase(rap1,complex,[rap1,'-',gtp], 'Rap1-GTP',r).
phrase(requirement, need2, [requirement, for], need,r).
phrase(ser, smallmolecule, [ser, 19], 'Ser 19',r).
phrase(ser, smallmolecule, [ser, 23], 'Ser 23',r).
phrase(serine, substance, [serine, residues], 'serine residues', r
).
phrase(src, domain, [src, homology, 2], 'Src homology 2',r).
phrase(src, domain, [src, homology, 3], 'Src homology 3',r).
phrase(srebp,protein,[srebp,'-',1], 'sterol-regulatory element bin
ding protein 1',r).
phrase(srebp,protein,[srebp,'-',2], 'sterol-regulatory element bin
ding protein 2',r).
phrase(sterol,protein,[sterol,'-',regulatory,element,binding,prote
in,1],'sterol-regulatory element binding protein 1',r).
phrase(sterol,protein,[sterol,'-',regulatory,element,binding,prote
in,2],'sterol-regulatory element binding protein 2',r).
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phrase(t, cell, [t,'-',dr7], 't-DR7',r).
phrase(t, cell, [t,'-',drt,'/',b7,'-',1],'t-DR7/B7-1',r).
phrase(t, cell, [t,cell], 'T cell',r).
phrase(t, cell, [t,cells], 'T cell',r).
phrase(t, complex,[t,'-',cell,receptor],'T-cell receptor',r).
phrase(t,cell,[t,'-',dr7, cells],'t-DR7 cells',r).
phrase(t,cell,[t,'-',dr7,'/',b7,'-',1], 't-DR7/B7-1',r).
phrase(t,complex,[t,'-',cell,antigen,receptor],'T-cell antigen rec
eptor',r).
phrase(threonine, aminoacid, [threonine, 229], 'threonine 229', r)

phrase(transcription, protein,[transcription, factor], 'transcript
ion factor',r).
phrase(trypan,smallmolecule,'trypan blue',r).
phrase(wt,protein, [wt, akt], 'WT Akt',r).
phrase(zap, protein, [zap,'-',70],'ZAP-70',r).
phrase(zdevd,smallmolecule,[zdevd,'-',fmk],'zDEVD-fmk',r).
phrase(il, protein,[il,'-',3],' interleukin-3',r).
wdef(ab, complex, antibody).
wdef(actin,protein,actin).
wdef(activated, state, active).
wdef(active, state, active).
wdef(ad,disease,'Alzheimer''''s disease').
wdef(agc,protein, 'AGC').
wdef(akt, protein, 'AKT').
wdef(anergic,state,inactive).
wdef(anergic,state,inactive).
wdef(anergy,state,inactive).
wdef(antibody,complex,antibody).
wdef(antigen, substance, antigen).
wdef(aop, protein, 'Aop').
wdef(apoptosis,process,apoptosis).
wdef(bad, protein, 'BAD').
wdef(c3g, protein, 'C3G').
wdef('ca2+', smallmolecule,'Ca2+').
wdef(cas, protein, 'Cas').
wdef(caspase,protein,caspase).
wdef(caspase,protein,caspase).
wdef(cbl, protein, 'Cb1').
wdef(ccrsrh,protein,'CCRSrh').
wdef(cd28, protein, 'CD28').
wdef(cells, structure, cell).
wdef(cholesterol,smallmolecule,cholesterol).
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wdef(cpp32,protein,'CPP32').
wdef(crkl, protein, 'CrkL').
wdef(ctf,substance,'COOH-terminal fragment').
wdef(cytokine, smallmolecule, cytokine).
wdef(cytosol, structure, cytosol).
wdef(djnk,protein, 'DJNK').
wdef(djun, protein, 'DJun').
wdef(dynamitin,protein,dynamitin).
wdef(erk, protein, 'ERK').
wdef(eto,smallmolecule,'ETO').
wdef(etoposide,smallmolecule,etoposide).
wdef(fad,disease,'familial Alzheimer''''s disease').
wdef(fyn, protein, 'Fyn').
wdef(gdp, smallmolecule,'GDP').
wdef(gelsolin,protein,gelsolin).
wdef(gp120,protein,'gp120').
wdef(grb2, protein, 'Grb2').
wdef(gst, protein, 'glutathione S-transferase').
wdef(gtp, smallmolecule,'GTP').
wdef(hsp70,protein,'HSP70').
wdef(human, species, human).
wdef(ikk, protein, 'IKK').
wdef(inactivated, state, inactive).
wdef(inactive,state, inactive).
wdef(jnk, protein, 'JNK').
wdef(jnk, protein, 'JNK').
wdef(jnk2, protein,' JNK2').
wdef(kap3,protein,kap3).
wdef(kdakt, protein, 'KDAkt').
wdef(kinase,protein, kinase).
wdef(kinectin,protein,kinectin).
wdef(klc,protein,klc).
wdef(lamin,protein,lamin).
wdef(myosins,protein,myosins).
wdef(nmdar,protein, 'NMDAR').
wdef(nmdar2b, protein, 'NMDAR2B').
wdef(ntf,substance,'NH2-terminal fragment').
wdef(p70s6k, protein, p70s6k).
wdef(p78s6k, protein, p78s6k).
wdef(parp,protein, 'poly(ADP-ribose)polymerase').
wdef(pdk1, protein, 'PDK1').
wdef(peptides, protein, peptide).
wdef(pkb, protein, 'PKB').
```

	206	979	-178	-352	-36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	-12	-255	97
	-76	-10390	-4298	-732	-1329	2508	-279	*	*											
13	1891	484	159	350	1092	-1	939	-607	452	-798	2975	440	751	-478	271	649	-518	125	545	2395
	206	979	-178	-352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
	-53	-10402	-4831	-732	1329	-2638	-253	*	*											
14	-1544	117	99	-433	1201	-927	779	-558	-17	-318	-25	-1196	812	225	-301	-421	440	735	-2569	653
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	20	-10421	-6282	-732	-1329	-2245	-342	*	*											
15	-271	-1402	122	84	621	-135	786	-1396	-125	16	-836	-1064	657	-830	-798	-173	82	811	558	618
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-23	-10502	-6072	-732	-1329	-3329	-151	*	*											
16	-1475	-1395	305	1025	1081	360	-400	-870	-768	-809	-3051	695	613	-548	-114	-1142	151	-98	1927	-111
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-41	-10494	-5199	-732	-1329	-3725	-113	*	*											
17	-945	24	278	129	1415	-574	164	-1466	-164	515	-238	833	463	-210	-2677	-785	-979	905	-25	-2438
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-118	-10455	-3687	-732	-1329	-3067	-183	*	*											
18	-903	83	828	842	1676	-1211	-1689	519	-65	-698	-2951	-483	349	886	-841	-1224	-1664	193	590	-247
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-58	-10373	-4702	-732	-1329	-3019	-190	*	*											
19	-604	-182	-2092	-158	1851	-1895	-84	840	856	-219	-2944	-188	607	-143	-763	-473	290	-2187	1413	114
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-2	-10365	-11365	-732	-1329	-2675	-246	*	*											
20	-946	873	129	-185	1399	-1954	-294	255	250	513	-1340	-2446	100	-1248	1200	-2351	775	-926	635	-188
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-2	-10435	-11435	-732	-1329	-2639	-252	*	*											
21	-985	-1396	77	-695	1037	-2004	-205	-216	636	647	-3052	1080	541	-171	-168	-2430	51	-405	-2630	1250
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
	-10	-10495	-7334	-732	-1329	-2652	-250	*	*											
22	-2205	-1431	391	417	1650	-2038	1141	-697	-144	490	1149	-706	284	-2483	-2077	-1155	-661	295	282	1418
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-52	-10537	-4839	-732	-1329	-3319	-152	*	*											
23	190	-1396	119	-627	1701	-2003	-73	-2084	265	55	-112	-956	648	617	937	-2429	-320	-172	-2630	746
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-2	-10494	-11494	-732	-1329	-2740	-234	*	*											
24	-1493	461	222	960	1719	-1229	496	13	-767	524	-1910	-2576	-387	-194	758	-1633	-991	233	-2667	246
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10538	-11538	-732	-1329	-3374	-146	*	*											
25	-1957	599	-335	119	937	-389	-1832	-204	849	-272	-471	-332	235	-612	925	-1335	21	344	-2672	1054
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-29	-10545	-5725	-732	-1329	-3560	-128	*	*											
26	-472	134	-420	-549	1604	-2022	348	-454	826	46	-155	711	-224	874	16	-2448	-1125	-215	-2649	1130
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-38	-10517	-5292	-732	-1329	-2966	-198	*	*											
27	-499	-1408	982	-2739	1396	-2015	-48	-365	-347	493	1123	-2551	188	1109	384	-317	-2360	-1741	-2642	1604
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-75	-10508	-4318	-732	-1329	-2826	-219	*	*											
28	-2151	-1378	-417	288	1496	-1985	-15	-869	-693	624	-1250	699	483	408	440	-1438	-2330	-465	-2612	2022
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-2	-10472	-11472	-732	-1329	-2865	-213	*	*											

29	324	-1411	115	185	793	-2018	422	-1214	616	339	-3067	-1268	646	1078	-112	885	-599	-436	-2645	897
	206	979	178	352	36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	-12	255	-97
	-56	10512	4750	732	-1329	-2887	-210	*	*											
30	-274	2097	1345	829	-597	-954	-1788	-963	-681	-469	-1882	-1739	700	790	678	-776	268	523	-2628	-2419
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-73	-10491	-4354	-732	-1329	-2901	-207	*	*											
31	-1182	222	623	536	461	-834	-1758	954	135	886	-3020	-887	-413	598	-2678	-1444	-2	-756	613	596
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-31	-10456	-5599	-732	-1329	-2527	-275	*	*											
32	1196	1488	1029	-163	-1851	-1234	-36	942	-1936	2	-3051	454	605	557	-870	-373	-271	373	-2629	810
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-60	-10493	-4638	-732	-1329	-2619	-256	*	*											
33	-934	478	634	-224	-756	-692	-1785	-479	-219	-175	443	725	1139	780	829	-1023	750	-851	-2625	-2467
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-69	-10489	-4442	-732	-1329	-2710	-239	*	*											
34	147	-1374	649	479	630	47	1225	27	49	-1018	4	-903	-935	147	330	-1376	916	-1204	-956	9
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-91	10467	-4043	-732	-1329	-2343	-317	*	*											
35	-2141	-1368	296	-86	1186	-30	-344	-919	-611	-13	-1005	-1858	478	760	406	-394	-21	-139	-2602	1782
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-73	-10461	-4366	-732	-1329	-2342	-317	*	*											
36	-677	600	1527	-213	476	-1985	65	294	-519	672	-3033	-1348	-953	882	-868	-2000	672	-311	-2611	608
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-32	-10473	-5578	-732	-1329	-2667	-247	*	*											
37	580	-1395	-438	-192	505	-604	185	45	-1156	979	-3050	-2538	-163	636	349	-1313	201	137	-2629	172
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	12	255	97
-	-47	10493	-4984	-732	-1329	-3697	-116	*	*											
38	-418	1347	739	-552	592	-203	-59	226	4	615	-3012	-1923	-86	862	245	-1556	24	1123	247	130
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
-	-2	-10447	-11447	-732	-1329	-3212	-165	*	*											
39	-873	2186	816	899	-809	-560	-353	-194	-967	-222	137	-2520	-529	1020	-423	280	-833	-447	-2610	1012
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-2	-10471	-11471	-732	-1329	-2695	-242	*	*											
40	-1805	-781	613	-935	1139	-801	1220	-497	-25	-2	-3074	-2562	850	641	-1550	-13	-562	-430	-2652	2131
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10521	-11521	-732	-1329	-2661	-248	*	*											
41	-381	1420	-492	-1975	-271	-1273	592	-86	263	96	354	-687	-561	636	266	-1199	875	256	-2689	1473
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
42	289	1850	131	-924	-1030	-2062	-283	-2479	47	905	-2917	-2599	509	1531	966	-1769	-6	-2446	-2689	991
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
43	-171	583	-660	-1238	-1172	-2062	-661	767	-1092	903	-3111	-1081	-277	1090	898	-1064	81	204	-2689	1310
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
44	-965	1662	-862	-152	-604	-627	414	-804	-869	383	-145	417	-2394	1951	265	-268	-1336	-113	-2689	1314
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
45	374	1081	-785	25	1187	-2062	-51	-3070	192	695	-3111	-572	-2394	1107	-930	338	-385	15	-2689	778
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

.	1	-10565	-11565	-732	-1329	3499	-134	*	*										
46	566	304	673	360	1082	-969	-11	-471	-1427	1512	3111	-482	2394	602	87	1503	-2042	834	2689	825
	206	979	-178	-352	36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	12	-255	97
-	-60	-10565	-4635	-732	-1329	-3499	-134	*	*											
47	418	21	-2564	-976	-1216	-187	-1800	-3020	-388	739	-1961	-243	-978	1516	-448	-2439	533	794	-2640	2302
.	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10506	-11506	-732	-1329	-3675	-118	*	*											
48	460	1406	160	95	2421	608	-1800	142	-202	858	-389	-2549	-2344	1727	-245	-443	-762	-660	171	-2482
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-24	10506	-5995	-732	-1329	-2459	-290	*	*											
49	-1271	-1437	1048	-1123	339	-813	346	50	-739	-33	-360	-2580	-2376	2048	579	-678	-550	205	-2671	1284
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10544	-11544	-732	-1329	-3002	-192	*	*											
50	666	746	-1057	-432	-2470	-1106	520	-575	335	764	-3111	-2599	-2394	966	422	-520	486	-357	-2689	1407
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
.	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
51	-708	1749	-381	-152	-2470	76	-1849	-785	411	105	-1257	-224	-23	1633	403	63	-325	-398	-2689	236
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
.	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
52	360	654	897	866	-2470	-412	276	184	-740	-831	-3111	62	385	248	-645	-1566	-966	1	1788	1039
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
53	629	737	922	-152	-883	-244	124	905	-1007	673	-640	-445	-504	301	-237	-221	-2408	-832	-2689	-716
.	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
54	430	893	-1901	-245	-106	-1397	-1849	1214	-1446	358	372	-1027	-771	420	-58	154	-81	188	-2689	872
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.	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
55	-416	955	-950	532	446	463	818	-1782	535	498	-353	-626	-967	218	-1587	532	-1500	-812	-2689	1059
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
56	-250	933	-182	-129	-1635	971	173	139	-729	626	-1371	106	-216	-112	-25	274	-812	-1094	-2689	429
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.	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
57	149	1050	501	692	-2470	806	592	-1124	-15	86	-1327	-1807	-224	-703	510	-532	-803	314	-2689	-84
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
58	561	-104	725	-133	-815	-931	1260	177	-45	851	-438	-1174	-527	-473	-5	-479	-2408	-1254	-2689	1305
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
59	989	973	67	-1693	947	-62	900	-397	-1003	-91	-2656	-948	199	1084	-2069	-783	-1677	-703	-2689	1800
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-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
60	-187	1718	336	922	-32	-1381	-24	-458	-328	689	-3111	-1774	796	-1113	-2769	202	-633	-162	-2689	783
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-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
61	235	1587	-177	-412	548	-222	1278	-3070	-1524	287	-3111	-1315	307	1431	-354	-67	-83	-452	-2689	583
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-89	-10565	-4081	-732	-1329	-3499	-134	*	*											
62	698	-1382	572	-74	-1677	476	732	-2996	-267	930	-304	-1352	-1319	-632	-1251	99	255	-1593	-2616	1295

	206	979	-178	352	-36	372	585	-635	438	-130	677	-164	41	-73	-335	54	27	-12	-255	-97
	-2	-10477	11477	732	1329	2200	-354	*	*											
63	203	1155	784	670	629	117	1036	-853	-966	996	-3111	-531	-619	816	-897	519	266	1159	2689	2531
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	335	-54	27	-12	-255	-97
	-50	-10565	-4917	-732	-1329	-3499	-134	*	*											
64	759	338	-522	609	2429	-687	1486	-1315	359	681	-3070	-1182	-987	-421	-2728	442	-156	44	-2648	672
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10516	11516	-732	-1329	2608	-258	*	*											
65	974	-1455	84	183	-2470	-49	-163	-560	-446	773	-1767	-278	-416	421	-1832	207	-372	-141	-2689	435
-	206	979	-178	-352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
66	869	73	53	-218	-883	-312	235	-385	-827	211	1454	-947	265	395	-1852	448	-1307	-1321	-2689	1346
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-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
67	530	-1409	906	696	346	-831	-1849	-132	333	810	235	-1312	-610	-128	-2069	-212	-458	-476	-2689	1162
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-	-50	-10565	-4899	-732	-1329	-3499	-134	*	*											
68	-335	-37	-2572	239	-823	-415	-1808	-811	-97	1312	361	-819	518	684	-533	-97	-2367	174	-2648	857
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	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
70	1036	647	514	-121	-314	483	-1849	-375	12	32	-3111	-2599	79	-1	-1033	262	-1491	-904	-2689	1300
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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71	1010	368	337	-829	1366	-542	1849	-42	444	-163	121	-2599	-673	744	-1209	-7	-609	-2446	-2689	1085
	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-10565	11565	-732	-1329	-3499	-134	*	*											
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-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
73	192	-816	663	827	-803	-25	-1849	-1015	-59	767	-2917	-1344	-1350	1458	-1952	-1280	-1433	681	-2689	1025
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-	-1	-10565	-11565	-732	-1329	-3499	-134	*	*											
74	113	-752	832	-1098	-1045	-684	-101	-870	-1003	1356	-428	-356	-57	905	-1262	-358	-1464	-57	-2689	952
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75	297	1131	465	-474	-602	274	479	-606	-550	-146	-3111	-1032	851	1288	511	-395	-1464	-346	-2689	56
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76	110	-1418	102	1055	-2434	-1360	93	-413	827	6	-652	-862	958	-846	628	-920	-287	-1172	-2652	1119
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-76	-10521	-4296	-732	-1329	-2666	-247	*	*											
77	-2167	-806	991	605	639	186	964	-3009	249	166	-1593	-701	-1510	1126	-696	-549	-41	-864	-2628	1470
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-	-66	-10492	-4511	-732	-1329	-3690	-116	*	*											
78	-1127	-1340	437	-2672	278	668	454	-80	220	-118	-2996	-2484	-189	724	205	73	133	675	-1234	640
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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79	-414	490	839	635	-336	914	266	-1919	202	-142	188	-2457	1287	-464	-2628	-2347	-71	-40	246	171
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-	-39	-10395	5261	732	-1329	-2683	-244	*	*											
80	-566	-1287	946	678	229	-196	1535	-1964	20	-1494	40	574	525	768	-1489	-1134	-326	-93	-2572	1056
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-55	-10425	-4757	-732	-1329	-3840	-104	*	*											
81	-904	-1294	925	353	-884	-322	875	188	883	262	-565	187	811	-640	-874	-1066	-2217	389	-2528	789
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82	488	1244	748	1210	-2260	-1143	862	-2859	122	-357	-2900	747	361	-1079	-804	-135	-117	-222	683	323
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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83	-1102	-1307	-1216	870	-740	701	94	515	285	-628	-433	-2451	310	1477	-831	-343	-972	-56	-2541	1048
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84	-2009	141	-386	1064	98	-526	1401	-1748	-78	-559	920	311	-2174	414	-608	441	658	329	636	-1264
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85	2004	600	289	-77	-2246	-626	1465	-53	602	377	522	-706	501	-270	-210	-681	-880	273	859	1256
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86	-680	404	681	-1141	229	-1075	1396	-432	763	413	-2850	-882	153	-2246	-356	-141	469	-130	-2428	1155
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-	-25	-10248	-5947	-732	-1329	-3438	-140	*	*											
87	993	-1205	729	554	260	-85	-1599	-335	1342	-1161	-181	-46	-52	-443	545	367	-1510	303	168	-829
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88	1434	-1245	-306	43	-1452	-780	335	-1199	393	368	-12	-351	171	291	271	123	39	1060	626	28
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-	-73	-10311	-4368	-732	-1329	-1620	-568	*	*											
89	396	698	136	205	835	-1181	456	-56	-717	-395	-1239	-237	-632	751	-2692	-255	-1360	867	858	1237
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90	1770	1423	-105	542	813	518	-399	-1460	-23	921	-774	-28	138	675	-333	-1345	-740	-265	239	237
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-46	-10527	-5025	-732	-1329	-3070	-183	*	*											
91	-2000	651	-173	697	558	-678	769	-648	-692	368	90	683	906	639	-814	-393	-699	-36	468	-954
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-39	-10504	-5276	-732	-1329	-2902	-207	*	*											
92	-288	-1401	-73	773	-816	-1086	159	-241	1958	55	-3056	-1098	-540	-380	185	-867	-916	-2392	875	989
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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93	-885	-1433	-1831	318	-845	-1596	887	-60	926	-65	199	-661	598	858	1238	-804	-268	-1158	1739	-86
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-105	-10539	-3850	-732	-1329	-2445	-293	*	*											
94	-279	56	408	990	1553	-741	-687	-1509	750	-526	598	507	-302	-1042	521	-938	-1081	-211	-2630	259
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95	232	1257	-690	477	1494	-1985	1307	-997	53	382	1300	-881	-1297	710	794	-2411	-1073	-990	-2612	-967
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	2	10473	-11473	732	-1329	3753	-111	*	*										
96	277	74	1024	194	793	937	1019	96	-409	274	3034	-1327	1332	1059	463	255	638	251	2087	1264
	206	979	-178	352	36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	12	255	97
	-31	10473	-5614	-732	-1329	2550	-270	*	*											
97	838	1406	-2563	885	-771	1086	852	112	1405	21	1114	-563	527	69	1513	1604	-212	248	257	175
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98	-1658	-1401	-501	417	-2416	1771	533	-445	1330	-932	640	-1480	890	723	-1328	1153	-271	282	-2635	283
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	335	-54	27	-12	-255	-97
	44	-10500	5097	-732	-1329	-3694	-116	*	*											
99	182	89	-656	486	120	-1537	-1760	-717	724	431	943	193	156	-416	149	-49	-1067	264	-53	-1237
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-	101	-10459	-3903	-732	-1329	-2339	-318	*	*											
100	860	486	-563	-33	-2372	-1964	108	-451	118	648	-1225	-2500	-259	1173	547	-610	-365	20	-555	556
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	-76	-10451	-4314	-732	-1329	-2299	-328	*	*											
102	-1362	212	829	-951	-918	-1446	161	-755	127	1027	476	-528	-954	-386	760	853	-345	-2340	10	769
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	-154	10470	-3316	-732	-1329	-3579	-126	*	*											
103	-828	-1256	241	1342	-2271	-1044	1495	-276	1462	-474	816	-2399	50	54	-881	473	-2208	-1178	620	-1330
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-110	-10326	-3785	-732	-1329	-3153	-172	*	*											
104	-948	-1207	420	902	272	-617	681	-1361	536	20	1242	-2350	-2145	458	-38	683	503	1040	2441	898
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	-97
-	-77	-10266	-4295	-732	-1329	-1765	-503	*	*											
105	150	-1333	375	292	-140	-1286	-1727	336	606	175	486	-2476	-390	-108	656	-1356	138	466	594	359
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-	-85	-10515	-4148	-732	-1329	-2251	-340	*	*											
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111	-7	-1555	-249	760	-602	-729	1103	-1438	-48	818	-1413	-543	-755	1309	774	-711	-126	-1520	-503	-524
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	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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123	-69	-1617	-274	347	376	444	-520	-988	172	38	430	751	-696	-861	-1187	52	-1320	291	1520	589
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	1	10818	-11818	-732	-1329	-2494	-282	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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125	-446	-1669	-221	-450	-1211	-788	-2063	-114	504	596	-1207	1310	-644	1906	-2862	-118	-206	-523	-2903	-54
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126	-605	-1669	-1140	358	339	-1117	-2063	-3283	-451	856	1623	-101	-130	776	492	511	522	-2032	-2903	-167
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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127	-514	-1669	-194	1415	571	-636	590	-1385	63	-963	223	-522	79	895	-870	-86	877	-1234	-2903	298
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-	-1	-10898	-11898	-732	1329	-1885	-456	*	*											
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	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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135	-768	93	1070	308	1053	-28	-2132	406	437	-130	48	1027	-1307	-127	-761	-369	-893	-72	-2972	1379
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142	-338	980	341	-859	-215	-528	115	-950	-574	983	-242	-1844	-35	-2037	-780	-1193	-686	889	-101	1946
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143	-1925	369	-89	-1743	-511	1227	424	-30	673	-1039	230	-1010	1271	-2723	-454	-976	-1440	579	-2905	1705
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145	23	-10797	-6034	-732	1329	-2680	-245	-1421	1047	-974	250	-2570	1051	-237	2665	-1271	74	234	1166
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147	-62	-742	-303	-1076	451	-97	2730	562	838	293	-1917	188	-2443	-2557	-930	-1002	1011	214	607	-1574
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	-	79	-10627	-4245	732	-1329	-3404	-143												
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	-	38	-10503	-5293	-732	-1329	-3104	-178												
150	-275	-1392	3	-912	1586	-1999	581	-252	-1793	-3047	278	-800	-604	630	194	-1081	802	-2626	-600	
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152	446	-1228	-299	-513	280	721	-1681	-543	1471	-2943	-1625	-2225	-1031	-1468	-868	-1498	655	-2521	-485	
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	-	71	-10356	-4399	-732	-1329	-4024	-92												
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154	-494	-1035	685	-562	-2050	1453	-1429	74	446	-287	872	-1973	-2034	-2349	-456	-334	943	-2269	-2111	
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163	403	1475	-1139	-2027	-1711	1039	-1090	845	-321	-291	-2352	-622	-1634	-1746	2010	1969	-1648	241	1930	-1772
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-	-110	-9606	-3792	-732	-1329	-4789	-53	*	*											
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-	-101	-9499	-3912	-732	-1329	-4852	-51	*	*											
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-	-320	-8402	-2353	-732	-1329	-5200	-40	*	*											
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-	-624	-8073	-1525	-732	-1329	-5256	-38	*	*											
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-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
-	*	*	*	*	*	*	*	*	*	0										

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        -3892      *   -101
     1    796    224   -933  -1107   -791    345   -170  -1390    370   -229  -1432    404   1515   -828  -1090    -39   -728   -767   1428    633
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -9  -7945  -8945   -732  -1329  -3457   -138  -3892      *
     2    256    153  -1005   -458    443    771   -242  -1462   -389   -957  -1503   -991    148   -900  -1162    685   1250   -543  -1081   1305
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -8  -8030  -9030   -732  -1329  -4178    -82      *      *
     3   -410    140  -1018  -1192    364    292   -254  -1475    870   -345  -1516  -1004   1542    520    110   -122    337   -852  -1094    465
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -8  -8055  -9055   -732  -1329  -4382    -71      *      *
     4    709    140  -1018   -753    472   -467   1129  -1475    452   -215    151  -1004    353   -912  -1174    673     66   -852    954   1023
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
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     5    765    112  -1045  -1219    259   1067   1221  -1502   -429   -288  -1544  -1031    371    -63  -1202   -185    763    -62    687   -964
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     6   -296     47  -1111   -579    345    129   -347  -1568   -495    457   -540  -1097   1661    489  -1267   -254    832   -945  -1187    544
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     -     -7  -8187  -9187   -732  -1329  -2241   -343      *      *
     7    238    -56  -1213  -1387    826    500    136  -1670   -597    133  -1711  -1199   1534    904  -1370     10   -408   -282  -1290    766
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     -     -7  -8317  -9317   -732  -1329  -3132   -175      *      *
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45	-502	1983	-1311	-283	-1168	-760	-547	-1768	1501	161	-1809	-634	-89	1109	-1467	205	-73	226	-1387	176
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-	-78	-8478	-4319	-732	-1329	-2699	-241	*	*											
46	-264	-131	-1289	-1463	-1146	-738	-525	-1746	58	415	-1787	-1275	-475	603	-1445	1749	615	-34	1973	-1207
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-	-85	-8431	-4196	-732	-1329	-2786	-226	*	*											
47	406	-111	-1269	-990	-297	-718	-505	-1726	44	252	-1767	-1255	-586	37	-1425	16	-121	1642	1487	1045
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-76	-8409	-4370	-732	-1329	-3178	-169	*	*											
48	61	1314	-1230	-1404	-415	-680	-467	-1687	732	-123	192	377	-787	-1124	-1387	674	1402	-67	1824	-1148
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8333	-9333	-732	-1329	-2049	-399	*	*											
49	-963	3110	-1348	-1521	-1205	-797	-584	-1805	954	-642	-1846	-614	438	-398	-1504	598	832	-205	1484	744
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-62	-8555	-4661	-732	-1329	-2949	-200	*	*											
50	-97	1704	-74	-1489	-1173	-349	-552	-1772	87	173	-1813	126	-119	-519	-1472	267	1686	-315	540	253
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-62	-8485	-4682	-732	-1329	-3064	-184	*	*											
51	-463	1118	-464	-1458	912	-733	-520	-1741	20	249	-325	-1270	1128	-1178	-1440	266	297	-297	-1360	1994
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-81	-8423	-4267	-732	-1329	-3169	-170	*	*											
52	362	2088	-858	-711	-380	-481	-481	-1701	-158	-537	-1743	547	212	64	-1401	1252	-157	174	-1321	212
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-71	-8344	-4484	-732	-1329	-3408	-143	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-69	-8270	-4528	-732	-1329	-3485	-135	*	*											

54	-315	1857	-385	-923	-1038	-630	-417	-1637	-564	1160	827	550	323	679	-1337	25	-339	-834	1278	-1099
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8205	-9205	-732	-1329	-3696	-116	*	*											
55	444	754	-439	-1354	908	-630	-417	-1057	539	1518	-1679	-519	-269	129	-1337	-1056	-976	-185	-1257	-1099
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-	-7	-8205	-9205	-732	-1329	-3696	-116	*	*											
56	-203	2112	-1181	-1354	-1038	-630	-417	-1637	1186	-182	1182	1636	-405	-1075	-1337	-1056	-81	504	1184	-1099
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8205	-9205	-732	-1329	-3696	-116	*	*											
57	-143	-23	-1181	-1354	695	-630	-417	-1637	1796	-421	-1679	-1166	-962	1183	-1337	533	623	47	-1257	-1099
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-	-7	-8205	-9205	-732	-1329	-3696	-116	*	*											
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-	-211	-8205	-2913	-732	-1329	-3696	-116	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-88	-7972	-4185	-732	-1329	-3825	-106	*	*											
61	461	1019	-1033	-1207	-891	-483	-270	-919	-417	-636	88	-1019	171	2454	-929	-909	933	-55	-1110	-951
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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62	46	2054	-1033	-1207	-891	-483	-270	-448	755	1400	-1531	-1019	-814	592	-1190	-52	-528	-502	-1110	-951
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63	1236	125	-1033	-1207	-891	-50	-270	-311	-49	-617	-1531	-1019	828	-355	-1190	-480	1097	-697	2591	-951
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-106	-7883	-3915	-732	-1329	-3876	-102	*	*											
64	-195	2183	-989	-1163	-846	-438	-225	-998	1707	-657	-1487	-975	-770	-883	-1145	-864	160	1473	681	-907
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7775	-8775	-732	-1329	-3960	-96	*	*											
65	-605	1556	-989	-1163	-846	-235	-225	-1446	66	-488	-1487	746	893	901	-1145	-273	1536	-94	404	-907
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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66	-101	3140	-363	-1149	-833	-425	-212	-1432	-359	143	-1473	-961	292	-870	-1132	508	-195	1020	-1052	-894
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-69	-7738	-4564	-732	-1329	-3996	-93	*	*											
67	-565	1100	-949	-1123	-807	-399	-186	-1406	-333	-690	-1447	-935	1798	-844	-838	-239	936	95	2283	1279
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-280	-7670	-2545	-732	-1329	-4034	-91	*	*											
68	-440	333	-825	-998	-682	-274	-61	-778	-208	514	-1323	-810	24	1	-199	-372	-129	1847	-901	-743
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

-	-103	-7341	-3997	-732	-1329	-4148	-84	*	*											
69	-410	364	448	-564	159	-243	-30	-431	-178	-182	-1292	-780	-575	1998	903	-178	-360	-628	-870	-712
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-33	-7251	-5973	-732	-1329	-4251	-78	*	*											
70	-403	370	-788	-961	-645	-237	-24	869	287	1016	-655	-774	-569	118	-944	561	-583	79	-864	-706
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-86	-7235	-4279	-732	-1329	-4274	-77	*	*											
71	-379	394	-764	-937	-621	-213	0	-392	-7	-583	-1262	-749	-544	-658	-70	700	823	115	3347	-682
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-210	-7154	-2960	-732	-1329	-4319	-74	*	*											
72	-314	459	-699	-872	-556	-148	65	-1155	378	-503	-1197	-684	-480	-593	-855	942	-494	1818	-775	-617
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-402	-6982	-2089	-732	-1329	-4478	-66	*	*											
73	-180	593	1278	-305	-422	-14	199	-1021	52	-516	-1063	-36	-345	-459	-444	879	-160	146	-641	-483
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-212	-6474	-2998	-732	-1329	-4535	-64	*	*											
74	381	644	-514	-688	-372	36	249	-971	102	-466	-1012	-500	-295	-408	-670	1646	-97	-348	-590	-432
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-	-170	-6305	-3348	-732	-1329	-4604	-61	*	*											
75	-76	697	-460	-634	-318	90	303	-917	156	-412	-958	-446	-241	-355	-617	-336	1973	-294	-537	-378
-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
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//

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ALPH  Amino
RF    no
CS    no
COM   [converted from an old Plan9 HMM]
NSEQ  0
DATE  Mon Mar  8 11:42:34 1999
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NULT       -4  -8455
NULE      595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM         A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y
          m->m   m->i   m->d   i->m   i->i   d->m   d->d   b->m   m->e
         -2810      *   -222
      1     24   -736    758   -258  -1752   1483   1437  -2351  -1278  -1846  -2392   -275    415  -1789  -2051    321  -1689   -541   2589   1402
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      -    -51  -9611  -4898   -732  -1329  -2060   -396  -2810      *
      2  -2098  -1325    820    263  -2340   1204   2775  -1076   -139  -2435  -2981    161   1306  -2377   -882  -1297   -865   -992   1731   1027
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      -   -122  -10407  -3640   -732  -1329  -1376   -702      *      *
      3  -2040  -1738   1576   -468  -2753    356   3944  -3352    108  -2847  -3393  -2881   -117   -926  -3052    -31  -2690  -2729   1991    -44
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -1 -10897 -11897   -732  -1329  -1654   -552      *      *
      4  -1634    249   -189  -1239  -2928   -829   3764  -1473   -494  -3022  -3569    211    -43  -2965   -174  -1528   -281  -2904   3856    467
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -    -15 -11096   6619   -732  -1329  -2782   -227      *      *
      5  -2704   1071  -1282  -1511   -966   1726   1193  -3545   -505  -3040  -3586   -194  -2869  -2983  -1295   -792  -1052  -1432   4722    745
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -    -44 -11116  -5086   -732  -1329  -3310   -153      *      *
      6  -1866    399    305  -1497  -1069   2078    553  -3521  -2448  -2026  -3562   -822    131  -2959   -575     95   -635  -1416   2139   2441
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      -    -34 -11089  -5433   -732  -1329  -2927   -203      *      *
      7   -264  -1913    665    136   -248   1501  -2307  -1473  -1003  -1782  -3569  -1328    127  -2965  -1284  -1413  -1287  -2904    449   3192
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      -     -1 -11096 -12096   -732  -1329  -2348   -315      *      *
      8   -838  -1960    630   -556  -2975   1822   -176  -1500    696  -1813   -584    407   1251   -109  -2433    162  -1000  -2951  -3194    879
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      -     -8 -11148  -7665   -732  -1329  -3799   -108      *      *
      9  -1279   -976   -584   -804   -979    554   3173   -679   2055   -739  -1932   -209   -839   -974  -1308   -107  -2906  -2945    429  -1366
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      -    -27 -11142  -5808   -732  -1329  -3144   -173      *      *
     10     15   1116   -698   -560  -2969    424   3235  -3568  -2495  -1410  -3610   1903    218    354  -1308   -797  -2906  -1944   1933    242
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      -     -1 -11142 -12142   -732  -1329  -3464   -137      *      *
     11  -1218    735   -822    347  -2975   1567   1089  -3574   -789   -248  -3615   2528  -1159  -1318  -3274  -1329  -2277   -579   1931   -950
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     12   -132    226    300  -2559  -2969   1967   1182  -3568   -377  -1809  -3610    684   1930    435  -1308  -2435  -2906  -1621   1225   -347
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      -     -1 -11142 -12142   -732  -1329  -2679   -245      *      *
```

13	-1238	-2001	418	1334	-3016	474	1189	-3615	211	-1220	-3657	-1180	2353	340	-1379	-1466	-1381	-1271	1291	-795
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-	-32	-11195	-5544	-732	-1329	-3719	-114	*	*											
14	-1935	-1972	-247	2067	-506	-198	2302	-714	-566	-1182	-3628	574	-65	533	-27	26	-2925	-2371	1179	-3048
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-	-1	-11163	-12163	-732	-1329	-2914	-205	*	*											
15	-1532	-1989	-855	51	-584	-1379	3397	-723	-653	-1299	-3645	172	1157	311	-1351	-800	-1861	-2981	3783	-3065
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-	-1	-11182	12182	-732	-1329	-3333	-151	*	*											
16	-1322	1176	-1153	-3326	-3010	-1807	2521	-1543	207	-786	-3651	-1171	-141	-1020	-1354	497	-1358	-1255	4727	-1014
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-	-8	-11188	-7695	-732	-1329	-2524	-276	*	*											
17	-945	1463	-1405	486	-3050	383	3156	-3649	1451	-1692	-3690	-956	756	-565	-2490	-1661	-846	-1099	2092	7
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-	-14	-11233	-6738	-732	-1329	-3579	-126	*	*											
18	-2796	947	276	-939	-801	-123	-102	42	2007	268	-3679	-238	-4	50	-1201	-1413	-379	143	-3257	448
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	-8	-11183	7658	-732	-1329	-3789	-108	*	*											
20	-1544	-403	-3141	-1094	2306	-195	-2378	377	219	-1209	-3639	212	1931	-1035	-3298	-24	-637	-702	1108	77
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11176	12176	-732	-1329	-2938	-202	*	*											
21	-1556	1196	-1365	-1332	-3016	33	-245	1658	256	-1875	-3657	445	2215	-237	-581	149	2953	5	3235	3077
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	255	97
-	-8	-11195	7677	-732	-1329	-1701	-530	*	*											
22	1268	1738	-75	2663	-3097	-53	-2476	1833	-696	-1075	-3738	-1415	-1331	843	-692	-377	278	246	3316	904
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	12	255	97
-	-23	-11267	-6029	-732	-1329	-3033	-188	*	*											
23	1809	1839	-794	2654	-3082	59	-325	-3682	1043	-1951	-595	1343	-812	1094	-3381	217	-986	-3059	-3301	-875
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11270	12270	-732	-1329	-2525	-275	*	*											
24	-1643	1678	-1454	-2187	-3099	1756	-2478	-1657	1918	-900	-3740	783	-58	347	-1282	-189	479	-3075	-3318	-3160
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-23	-11288	-6001	-732	-1329	-1411	-681	*	*											
25	-140	-2110	-561	542	-3125	2055	-1531	-834	75	-2055	-2090	418	687	806	-1293	-211	-318	-1601	-3344	-877
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11316	12316	-732	-1329	-1896	-451	*	*											
26	-1465	-2137	535	1501	-3152	-78	-1552	-353	-1080	-1199	-1353	859	257	1359	1466	-233	-555	-1636	-3371	-3213
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11346	-12346	-732	-1329	-1977	-423	*	*											
27	-2931	-2157	621	-2753	-3173	-2765	752	906	258	-816	-3813	83	544	2194	2245	-465	-2466	-1666	-3391	-408
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-22	-11370	-6065	-732	-1329	-2450	-292	*	*											
28	-576	-2137	75	-1927	-365	-2744	18	329	-2678	-1998	-3792	-513	-175	2953	-698	1614	-1502	-809	-3371	-3213
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11346	-12346	-732	-1329	-1977	-423	*	*											
29	-2931	-2157	-238	-980	-3173	-2765	-396	237	-284	-1475	-3813	-1347	2286	702	-1530	2054	-312	-950	-3391	-3233
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11370	-12370	-732	-1329	-2450	-292	*	*											
30	-608	-2157	64	-980	-3173	-1556	306	1281	574	-3267	-3813	-1670	2658	-3210	-1530	187	-1532	759	-3391	-3233

-	206	979	178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	-255	-97
	22	11370	6065	732	1329	2450	292	*	*											
31	-967	2137	1229	731	-3152	-2744	2531	1310	95	-144	-3792	518	727	162	3451	1744	881	1545	3371	462
	206	979	178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	255	97
-	-51	-11346	-4851	-732	-1329	-2571	-266	*	*											
32	-1614	-2087	2112	-1647	3103	-1713	471	1986	105	-512	-3743	1388	-510	-184	-3402	-970	1434	-1569	3321	6
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-24	11291	5939	-732	-1329	-2272	-335	*	*											
33	-955	-1118	1468	-792	-1100	-1462	1206	2243	233	-978	-700	-3231	-11	-1719	-1764	-154	-1434	605	-3321	-3163
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11291	-12291	-732	-1329	-2868	-212	*	*											
34	-1614	-2087	2078	-586	1438	-2695	539	209	216	-246	-2077	-1860	-283	574	-328	-2178	1641	-236	-1301	-842
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11291	-12291	-732	-1329	-1641	-558	*	*											
35	-642	-2137	290	-1365	149	-1948	1735	-937	758	-846	-2109	-351	-285	-387	-491	717	1935	-1063	378	-3213
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-23	-11346	-6026	-732	-1329	-1977	-423	*	*											
36	-394	2137	918	-114	26	-2744	3237	-353	146	-2088	-3792	221	-425	-1357	-804	-363	989	-1482	237	307
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-29	-11346	-5681	-732	-1329	-1977	-423	*	*											
37	1012	2131	-119	-2249	-362	-1523	699	-1087	-382	-740	-3787	-511	-1343	1309	-626	467	1893	-1112	239	-910
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-23	-11341	-6023	-732	-1329	-2666	-247	*	*											
38	1505	-2110	-167	-2715	-3125	-503	946	-570	1114	-350	-3766	-1874	-1234	351	-186	-496	7	336	-3344	997
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-24	-11316	-5982	-732	-1329	-2171	-362	*	*											
39	-469	-2110	-97	-2715	-2266	-841	2180	-2815	1977	-138	-3766	-543	-391	35	38	342	1467	-1293	3344	1677
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-38	-11316	-5301	-732	-1329	-1896	-451	*	*											
40	-599	-2105	2063	-3437	-441	-1506	181	-3720	-1135	-501	-3761	-110	265	-937	-599	-114	-2413	-372	252	2913
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-	-46	-11312	-5014	-732	-1329	-1551	-602	*	*											
41	-231	-2094	2484	-3425	-1112	-1637	-2488	-1630	-91	-487	-569	575	1494	136	-3408	277	-229	-1091	-3328	-3170
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-24	-11298	-5956	-732	-1329	-1988	-419	*	*											
42	574	90	-960	-2709	-308	284	198	-3714	2	-196	-3755	-2399	2312	-1729	-62	958	-1647	-1	-3333	-3175
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11304	-12304	-732	-1329	-2257	-339	*	*											
43	-992	-2115	-518	-1149	-2272	-2722	-962	-1654	262	1265	-1000	-1189	319	515	-564	1906	-177	-1605	-14	-2134
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-24	-11322	-5984	-732	-1329	-2091	-386	*	*											
44	-479	-2115	-518	-711	562	-328	-331	-3729	1492	1622	-1342	-1283	-1424	636	-1676	102	-3068	-738	-3349	-358
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-24	-11322	-5984	-732	-1329	-2682	-244	*	*											
45	-1362	-2092	1419	-1650	-3108	79	-34	-1620	2175	-235	-3748	-3236	1937	-1334	-812	-277	-293	-967	309	1031
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-24	-11296	5942	-732	-1329	-2197	-355	*	*											
46	-923	-2092	-951	-901	-1336	-553	-296	-15	-319	618	-3748	-347	2147	258	-204	375	-696	-3084	1464	534
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-128	-11296	-3560	-732	-1329	-2785	-226	*	*											
47	-1705	-1959	384	-438	559	-2566	-96	193	-938	1571	-2009	-269	-309	-899	-1292	1077	-1029	-1689	60	648
-	206	979	-178	352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

-	-29	-11141	-5674	-732	-1329	-2410	301	*	*										
48	538	1966	-307	-3297	-316	-1294	540	63	-503	150	-3622	-437	1099	746	148	1303	131	1032	3200	199
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-	-63	-11149	-4559	-732	-1329	-1461	-651	*	*											
49	-1553	-2040	-1352	-660	104	-588	1542	256	-1044	-1036	-1296	520	-1213	429	-2529	1328	-1138	1735	977	-3116
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-	-71	-11236	-4401	-732	-1329	-2237	-344	*	*											
50	-738	-59	-1334	-1316	-3024	-835	-210	-1534	-2550	-80	-166	-901	-1195	225	-3323	1881	-209	118	-3243	2673
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-307	-11202	-2384	-732	-1329	-1407	-683	*	*											
51	-32	-811	-273	-1496	-2856	999	-153	-670	-2382	-1322	-431	1884	-1531	-951	-2265	-830	-2793	-1817	-3075	3232
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-422	-11016	-1983	-732	-1329	-3349	-149	*	*											
52	-1182	-1478	-76	315	-79	438	71	-2066	-889	9	-3134	1354	1258	-723	-2792	126	-337	-1799	1250	1585
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-160	-10589	-3258	-732	-1329	-2636	-253	*	*											
53	-31	-1510	1294	-569	511	665	956	-908	352	-140	-3166	1677	-2449	-2562	-1074	74	-1263	-879	488	-2586
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-13	-10628	6893	732	-1329	-2191	-357	*	*											
54	19	-1734	1491	-1100	-890	-429	1619	-3348	646	-862	-956	845	1027	-74	-437	-118	-151	-1061	-821	-606
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-28	-10893	-5758	-732	-1329	-915	-1090	*	*											
55	821	-2040	1754	-1269	-1073	-77	15	-706	-704	-949	140	847	103	504	-904	-366	434	-2025	-3274	99
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	-255	97
-	-14	-11239	-6774	-732	-1329	-1143	-870	*	*											
56	170	555	-3279	108	-357	147	-2515	-698	98	-669	-2088	-1789	-77	2254	-987	1092	207	319	3355	-3197
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	12	255	97
-	-23	-11329	6019	-732	-1329	-1793	-491	*	*											
57	1635	430	2528	-808	1006	-1430	-2535	4	675	-1517	226	732	-443	-999	-1678	-150	978	624	1320	3216
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-29	-11351	5699	-732	-1329	-1843	-471	*	*											
58	-542	15	-1604	11	315	-344	-2535	-61	-113	-1794	216	532	-32	-3193	215	220	1998	109	-505	-2142
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-148	-11351	-3360	-732	-1329	-2735	-235	*	*											
59	-1645	-995	519	-558	-351	-802	-293	-806	410	471	540	1332	-763	-1092	-503	1516	428	-1555	-3243	-941
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-	-45	-11206	-5039	732	-1329	-1356	-715	*	*											
60	-818	819	1444	269	532	-284	-325	-1360	-444	1413	-3727	-51	-1437	-317	-191	-831	876	357	-426	-3147
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-27	-11274	-5791	-732	-1329	-1526	-615	*	*											
61	-2872	59	-378	-514	-334	-852	1011	1859	-2144	-1042	-1300	643	-3037	-1140	1746	-1717	781	186	982	-2101
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-	-65	-11304	4508	-732	-1329	-1487	-636	*	*											
62	-1775	87	656	-1407	-313	-456	517	2077	-2138	-137	-152	1444	-3026	-24	-1448	-1693	-636	1110	726	-862
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11291	12291	-732	-1329	-2683	-244	*	*											
63	-2866	-2093	1437	-2214	-316	-828	579	-107	306	1116	-160	2516	-3031	-2257	-23	-415	-59	-812	-1291	-578
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-86	-11297	4116	-732	-1329	-2052	-398	*	*											
64	-860	-2022	1321	-3353	-1003	-830	641	-3637	-405	-373	-3678	3282	-2961	-180	-1333	-3055	363	666	-3256	-743
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-26	-11215	5817	-732	-1329	-2531	-274	*	*											

65	2795	-42	1598	3353	-3037	1640	1069	-1520	-1225	-2341	-454	2722	90	-3074	1333	1370	1101	92	3256	3098
	206	979	178	352	-36	372	585	-635	438	-130	677	-164	41	-73	-335	54	27	12	-255	97
-	-52	-11215	-4826	-732	-1329	-3122	-176	*	*											
66	-1450	-1968	-3126	-427	792	2220	2779	-516	-44	-3078	3624	-255	-1103	298	-418	-1615	-459	-667	-3202	3044
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-28	-11152	-5713	-732	1329	-1493	-633	*	*											
67	-38	-2062	-444	3393	644	-142	3521	-1577	-854	-646	-3718	-246	-1561	-381	-2026	1115	-928	205	-3296	-750
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	11261	-12261	-732	-1329	-2368	-311	*	*											
68	1258	446	487	-1643	2102	-669	847	-2799	-517	-2388	-2077	-1242	-2318	273	-3400	-62	1060	522	-3320	-3161
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-	-24	-11288	-5934	-732	-1329	-2274	-334	*	*											
69	-952	-1117	1413	-371	2574	-1314	1041	704	-1311	-856	-174	775	-506	-548	83	-967	-507	157	315	-838
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-24	-11288	-5934	-732	-1329	-1854	-467	*	*											
70	-1435	-2108	233	-569	-1130	-837	-324	-125	-669	-1749	1011	2132	-1307	1173	-2582	133	-1464	1591	-1312	-3184
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-47	-11314	-4986	-732	-1329	-1898	-451	*	*											
71	-1361	107	348	607	-1336	415	-292	-433	-1101	-519	-840	694	-3029	-170	-1428	-828	-993	2009	313	8
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-72	-11294	-4363	-732	-1329	-2786	-226	*	*											
72	-2790	-1074	11	1631	2312	1164	-2411	-204	-2558	-212	-2044	-680	-536	-523	-858	-1364	-71	-2446	-3251	-1478
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-53	-11208	-4802	-732	-1329	-2476	-286	*	*											
73	-1473	1990	1066	128	2432	25	-2384	-2736	453	-75	-3646	-719	343	-940	-1988	23	-535	-2425	980	318
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-55	-11177	4749	-732	-1329	-2145	-370	*	*											
74	-803	-1990	2823	-1091	-792	334	-2384	-3604	-999	372	-392	-136	-725	-3042	-1988	-565	691	-2981	-3224	-684
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-77	-11177	4285	-732	-1329	-1824	-479	*	*											
75	-575	-1997	2291	-2167	-2188	83	-1457	-3611	-264	-673	-3652	810	639	-3049	-1529	1227	-184	-1435	-3231	429
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-172	-11185	-3159	-732	-1329	-2139	-372	*	*											
76	-700	-1904	1671	2010	-676	-735	847	-1473	-570	-470	-3560	-295	-370	660	-1284	1836	-1020	-551	-3138	143
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-309	-11086	2378	-732	-1329	-2875	-211	*	*											
77	-238	-639	1365	-1363	-2698	30	-1036	-1343	84	-455	-549	330	-284	2715	-1440	111	-862	-2674	-2917	-2759
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-220	-10835	-2828	-732	-1329	-2628	-255	*	*											
78	-1227	-1596	2359	-735	-427	320	-1990	-1265	878	-542	1142	399	-914	-2648	613	-2030	-2548	-2587	-2830	1132
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10733	-11733	-732	-1329	-1664	-547	*	*											
79	480	-1846	-484	-2419	-2861	133	811	-2513	1916	-2956	-1769	-292	-187	232	-50	916	-2134	-691	-3080	1621
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-74	-11022	-4334	-732	-1329	-1111	-897	*	*											
80	1593	-1989	3147	-2590	-218	-250	-2383	-1114	-1234	-399	1046	-472	-138	-207	-552	-139	-900	1374	-3223	1106
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-8	-11182	-7685	-732	-1329	-918	-1087	*	*											
81	-697	-1141	-3282	-1706	-47	-104	-355	812	-738	1213	-2094	-805	-459	-731	-464	-628	-814	1514	575	85
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-46	-11333	5026	-732	-1329	-2755	-231	*	*											
82	-2058	-2080	-629	2	-88	-859	546	321	1106	1355	627	-3224	-1489	526	-423	-625	153	-162	-3314	-2105

	206	979	-178	352	-36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	-12	-255	-97
	22	-11283	-6097	732	-1329	-2550	-270	*	*											
83	-372	-2065	734	-973	-585	1665	-2459	-509	1592	-51	-520	-1212	-475	-798	-273	378	-130	-1269	3299	-3141
	206	979	178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	-97
	-1	-11265	-12265	732	-1329	-2088	-387	*	*											
84	-960	-2093	-181	-2705	-3108	2776	1648	-759	-2635	-821	-3749	-1250	-193	-1099	-1245	122	-550	-1772	-3327	-846
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-22	-11297	-6105	-732	-1329	-2220	-349	*	*											
85	-125	-2093	487	-3425	1176	2162	535	-1429	-1319	-624	-560	403	1575	-833	-1433	-1875	-1439	-3085	307	-847
	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-7	-11297	-7830	-732	-1329	-2220	-349	*	*											
86	-805	-2108	209	-1677	375	707	1292	-2814	-2650	1163	-2089	-1009	2100	-1247	-145	-3141	-575	-2100	-3342	890
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-13	-11314	-6864	-732	-1329	-2373	-309	*	*											
87	1027	-1126	60	-1014	-3118	-609	510	-1371	-1340	1592	-2082	-3247	828	-3155	-655	748	185	-594	2061	416
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-47	-11309	-4984	-732	-1329	-2459	-290	*	*											
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	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-19	-11261	-6272	-732	-1329	-1453	-656	*	*											
89	-1098	2120	423	652	160	1574	1167	-1396	-1801	-595	-1330	-133	73	-31	151	559	-23	-695	248	-12
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-52	-11328	-4838	-732	-1329	-2137	-372	*	*											
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	-1	-11283	-12283	-732	-1329	-2550	-270	*	*											
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	206	979	178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-11288	-12288	-732	-1329	-2869	-212	*	*											
92	-2064	-2086	1738	22	989	-1459	1826	-2248	30	1234	-552	-3229	-1274	22	1955	-967	83	-3077	-3320	-38
	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-1	-11288	-12288	-732	-1329	-2869	-212	*	*											
93	138	-2086	-1413	-3417	1392	-1459	1773	-81	42	1354	-3741	-1242	-814	546	506	-757	-2409	-208	315	-838
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-88	-11288	4082	-732	-1329	-2470	-287	*	*											
94	-589	-2001	-1048	-2169	-966	-1339	2360	1771	-56	-1173	-562	-3144	-987	2339	-1051	-99	-1590	-595	1398	-1467
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-110	-11190	-3781	-732	-1329	-1861	-464	*	*											
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	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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97	-2790	-2017	-861	159	1900	36	3775	-167	-1210	-916	-3673	-1823	-2955	-523	-674	-381	-1333	-403	433	-3093
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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117	137	-2067	-3225	33	59	-1049	1802	-444	1898	-979	-516	-1209	-3006	-3119	426	-3100	-1630	-774	-3301	2631
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118	500	-2091	-1108	-374	971	-1006	1935	866	-179	-535	554	-3234	-324	-3143	-433	288	-3043	702	-3325	2834
	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-24	-11294	-5937	-732	1329	-2384	-307	*	*											
119	2177	-1114	-1136	-978	735	-200	1009	-2248	-2613	-445	30	-1212	926	-3124	-3386	-915	-1477	184	-3306	650
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11272	-12272	-732	1329	-2221	-348	*	*											
120	1402	-2096	-3253	1706	1102	-676	1447	-423	-1105	65	603	-3239	514	-3148	-3410	-1186	-695	149	311	-843
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11299	-12299	-732	-1329	-2696	-242	*	*											
121	-1411	-2096	-1419	2215	-293	-2703	1689	-316	-1318	1199	-2090	651	-3034	-832	-3410	-1680	-3048	309	310	-843
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122	489	1130	-2505	176	-293	-2703	3277	-1009	-1318	1274	880	1025	-1280	-1732	-1431	-3129	-3048	591	311	-843
	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	24	11299	5939	732	1329	-2696	-242	*	*											
123	-404	-2072	-599	3403	-3087	-1432	3757	-209	-174	1038	62	-955	-3011	85	-1395	-1934	-658	51	1143	-3148
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-	-50	-11272	-4902	-732	-1329	-2798	-224	*	*											
124	-725	2022	-13	-1621	-742	-2629	1544	366	284	1394	-1306	98	-2960	-199	-1319	-1574	-2364	1674	431	-3098
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-	-1	-11214	-12214	-732	-1329	-1998	-416	*	*											
125	-307	-2072	-599	-1614	1330	-323	3199	301	204	-3182	-3728	-18	-1468	-3124	-3386	-1646	-1402	2068	-3306	898
	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	-12	255	97
-	-76	-11272	-4298	-732	-1329	-2221	-348	*	*											
126	-727	211	-1316	-1106	-533	-706	3576	-3637	-75	-1839	-810	84	-2961	297	-1327	-1582	-1336	195	3901	-55
	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-46	-11216	-5028	-732	-1329	-2515	-277	*	*											
127	-198	-2002	1379	-2160	445	-1152	-171	-3616	765	-1620	-234	2156	-385	571	-1058	-981	-1317	-2428	3955	428
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-30	-11192	-5616	-732	-1329	-2858	-214	*	*											
128	-825	-1978	735	-2613	-944	-1317	-1436	-3593	510	-312	-3634	2397	573	-939	-2484	151	597	-332	-3212	1099
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-229	-11165	2770	-732	-1329	-2472	-287	*	*											
129	391	-1814	-969	349	-822	-396	-2208	-3429	1126	-1754	-1807	405	55	-1056	-2295	330	2164	-1292	-3048	-564
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-455	-10982	-1890	-732	-1329	-989	-1011	*	*											
130	-2465	-1691	1175	247	-2707	-699	-2086	-1295	2211	-283	-1619	438	-504	-772	-2131	260	448	-2072	-2926	174
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-19	-10845	-6311	-732	-1329	-911	-1095	*	*											
131	285	-1975	527	-951	-901	-14	-2369	-3589	2217	-993	-3631	-1215	-413	-3027	-469	-1523	-1565	-2966	-3209	2768
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-	-41	-11161	-5182	-732	-1329	-2928	-203	*	*											
132	-750	-1942	488	-524	18	1173	-2336	-840	-2483	-361	-3597	97	-1118	-2994	-1222	788	-1869	-153	-3176	2756
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11122	-12122	-732	-1329	-2847	-216	*	*											
133	225	-1970	623	171	16	1778	-2364	-1451	-235	-590	-3626	-453	-2225	-2171	-3284	1226	-697	-198	-3204	-814
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-59	-11155	-4648	732	-1329	-2986	-195	*	*											
134	43	-1928	2097	-754	1764	-414	-2322	-317	-1996	-1062	-3584	-390	-2867	429	-3242	-52	-1231	147	-3162	1368

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-	-8	11109	7682	732	-1329	-2663	248	*	*											
135	664	-1974	-703	548	2409	398	-2369	-2134	-39	144	-1962	-3118	-398	3026	1317	15	-1432	-459	3208	594
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	-12	-255	-97
-	-1	-11164	-12164	-732	-1329	-3308	-154	*	*											
136	597	215	215	1329	12	1733	-2374	-1508	1236	-1824	-3636	-2281	-1169	-1219	-1320	-1209	-1531	-154	-3214	-3056
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-	-1	-11170	-12170	-732	-1329	-3645	-120	*	*											
137	1861	-1980	-235	-180	-422	-564	648	-1013	1885	-1161	-3636	-3123	-2918	236	-1320	-641	-1866	-738	-3214	115
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-64	-11170	-4543	-732	-1329	-2534	-274	*	*											
138	2132	-1971	350	-1536	331	-249	-2365	-1236	572	-479	470	-398	-1380	-1598	-3285	-969	-140	354	-3205	-3047
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11160	-12160	-732	-1329	-1629	-563	*	*											
139	565	-2056	27	-924	-1083	80	-2450	-1096	1017	-49	-3712	-3200	-2995	1166	-1412	142	-1596	1864	-3290	-3132
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-	-1	-11256	-12256	-732	-1329	-2581	-264	*	*											
140	-682	1303	422	-907	-282	-126	1486	-733	925	-186	-3723	-2363	-1106	2642	-2541	-289	-533	-323	-3301	-3143
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11268	-12268	-732	-1329	-2260	-338	*	*											
141	660	-2094	539	-290	-321	98	-1511	-952	-26	-419	-3750	-1272	1309	2150	-1648	-1031	-1458	248	-3328	-3170
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-	-7	-11299	-7805	-732	-1329	-3002	-192	*	*											
142	-1082	-2089	2039	-497	-3104	1053	-1505	-306	-465	-1292	-3745	-1458	2107	-2251	-1181	-1697	-1455	489	3323	-866
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-	-24	-11293	-5974	-732	-1329	-2124	-376	*	*											
143	-160	-2082	2008	-2692	-3097	2000	-525	104	-2139	-899	-3738	347	-508	-825	-747	-1947	733	228	1294	3158
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-	-1	-11285	-12285	-732	-1329	-1540	-608	*	*											
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-	-62	-11344	4588	-732	-1329	-2172	-362	*	*											
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-	25	-11281	-5912	-732	-1329	-1517	-620	*	*											
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-	-1	-11325	-12325	-732	-1329	-2006	-413	*	*											
147	459	-2140	1485	-990	184	-567	-82	989	-708	451	-3796	-1315	-3079	-353	-3454	-1744	-2455	2413	-3374	-2154
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-	-1	-11350	-12350	-732	-1329	-2468	-288	*	*											
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-	-23	-11350	-6024	-732	-1329	-2468	-288	*	*											
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-	-1	-11325	-12325	-732	-1329	-2006	-413	*	*											
150	-171	-2140	-3298	-447	2074	460	-2534	2232	-1381	-102	-2115	-3284	-1346	5	-1498	-3173	-764	525	-3374	-3216
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-	-23	-11350	-6024	-732	-1329	-2468	-288	*	*											
151	-542	-1145	-169	194	2539	-1671	-2512	-674	-1350	1250	1947	-1282	-772	199	-3432	-3152	-730	-696	-3352	-3194
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-	206	979	-178	-352	-36	372	585	-635	438	-130	677	-164	41	-73	335	-54	27	12	255	97
-	-106	-11278	-3831	-732	-1329	-1836	-474	*	*											
153	-1314	-2017	-2445	190	532	-757	-178	588	1897	-519	-435	-674	108	554	-1274	-3050	-1101	1500	-3251	-554
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11208	-12208	-732	-1329	-1479	-641	*	*											
154	-612	-2113	-736	436	-640	1370	-2507	-624	-442	-511	-3769	38	64	-782	-1462	-244	-1226	1855	-3347	-1530
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-	154	-11320	-3312	-732	-1329	-2683	-244	*	*											
155	61	-1979	96	-297	678	2115	-2373	-1535	-128	-1845	-3635	850	475	110	-3293	-179	-2290	-1149	-3213	144
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-	-49	-11170	-4915	-732	-1329	-943	-1059	*	*											
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-	-126	-11274	-3583	-732	-1329	-1357	-714	*	*											
158	-340	-2016	713	358	-400	-1207	-415	-3630	1990	-798	-1963	1729	-555	-266	-983	-76	-746	-734	-3250	-3092
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-	-32	-11031	-5530	-732	-1329	-764	-1282	*	*											
160	-671	-2092	-1420	375	-2256	61	-2487	-370	868	-182	-3748	404	2372	-242	-2573	-1620	-1373	-575	308	984
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-	-1	-11296	-12296	-732	-1329	-1935	-437	*	*											
161	-695	-2118	-179	-1430	829	1536	-2512	92	-141	1283	-2103	-1282	-438	199	-1473	-439	-135	-2527	-3352	-786
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-	-30	-11325	-5646	-732	-1329	-2587	-263	*	*											
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-	-1	-11294	-12294	-732	-1329	-2384	-307	*	*											
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164	181	-2118	75	-759	-344	-843	-330	330	1941	-895	65	-1500	811	-318	-1128	-1485	-1082	1082	-3352	-3194
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166	-885	-1098	1717	-1122	75	-2655	1449	427	-568	-250	550	-349	-1208	-1704	-1107	-638	-406	1691	-1291	-3123
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168	-38	-2072	-94	-907	-103	-1030	454	-201	-78	1182	134	-96	-3011	-1187	-922	-798	-154	1516	-3306	-807
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-	-25	-11272	5893	-732	-1329	2221	-348	*	*											
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-	-1	-11272	12272	-732	-1329	-2221	-348	*	*											
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173	-803	-2135	-1482	3466	-199	-103	-79	-1407	2110	-1532	-626	-348	458	-1752	-918	457	1592	-461	-3369	-789
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-	-1	-11344	-12344	-732	-1329	-2172	-362	*	*											
174	94	36	707	-748	-544	-843	424	-159	1786	-484	-3796	-3284	-1887	-1164	-480	-762	1944	-716	-3374	62
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11350	12350	-732	-1329	-2468	-288	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-29	-11350	5681	-732	-1329	-2468	-288	*	*											
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-	-51	-11350	4850	-732	-1329	-2468	-288	*	*											
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179	1548	-1139	805	-268	188	-1494	-569	-1455	-40	-2058	-3769	-1880	1676	-1739	-2588	-209	711	59	-3347	-592
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180	150	75	1846	-1874	2432	-2715	-324	-524	-565	-1036	-2089	-314	-90	-855	-725	-1004	865	-2100	-3342	-873
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181	-826	42	-185	-1451	2321	-257	-2524	-2274	-430	785	669	-1886	665	-348	-65	-2608	1066	-1187	-3364	-907
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-45	-11339	5028	-732	-1329	-2270	-335	*	*											
182	-479	807	964	-1646	177	-642	210	-3705	-603	280	-3746	1607	-974	-1726	-373	-346	1931	-1568	-3325	-3167
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-	-24	-11294	-5937	-732	-1329	-1569	-593	*	*											
183	-992	-570	1224	-1888	2342	-800	261	-1653	-2660	-753	-3774	2012	913	-1131	-1465	-217	-407	-1171	-3352	-3194
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-	-24	-11325	-5982	-732	-1329	-2006	-413	*	*											
184	-2892	-173	1557	-1683	2627	-843	502	-46	-2660	-212	-3774	-177	163	-2289	-1200	-695	-730	-738	-3352	1399
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-	-1	-11325	-12325	-732	-1329	-1593	-581	*	*											
185	-1056	289	2025	-88	580	-2768	-2555	-921	-917	552	-662	-1524	1965	-3213	-1257	-350	-1532	-2560	1143	-100
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-44	-11374	-5073	-732	-1329	-2339	-318	*	*											
186	-2438	953	308	-818	-285	-2278	-2512	-1565	-1811	787	-3774	-856	2385	-3170	687	271	230	-1114	274	-31

-	206	979	-178	-352	-36	372	585	635	438	-130	-677	-164	41	-73	-335	-54	27	12	-255	-97
-	-24	11325	5982	-732	-1329	-1593	-581	*	*											
187	-2456	824	2042	-2261	-1169	527	-2534	-870	-567	-13	-771	130	600	-79	1984	214	97	-1067	1516	727
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	-44	-11374	-5073	732	-1329	-2339	-318	*	*											
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-	-89	-11325	-4070	-732	-1329	-1593	-581	*	*											
190	-2851	-1117	-610	-1737	-661	-841	-2472	-3692	-480	1896	-3733	-415	2149	-809	-1405	-232	-668	-3069	338	564
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-	-81	-11278	-4208	-732	-1329	-1243	-792	*	*											
191	-871	84	-560	-110	-851	-774	-2487	-3707	-2144	254	-3748	-2384	2714	-2257	231	443	219	-3084	286	897
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-24	-11297	5970	-732	-1329	-1141	-872	*	*											
192	-1060	1523	138	1581	-1757	-1316	-363	-3755	-72	-1252	-3796	-389	852	-3192	-1002	1007	788	-1399	238	1155
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-110	-11350	-3775	-732	-1329	-1885	-455	*	*											
193	-510	254	179	-1403	-1126	-2673	-2460	-1644	-986	664	-3721	-1801	-232	-3118	-70	1911	935	-1588	1212	1135
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-287	-11268	-2475	-732	-1329	-1093	-913	*	*											
194	-2677	-1903	-590	-729	-52	-733	-228	-3518	-2445	1719	-3559	-3047	290	-714	830	-104	719	1463	92	1710
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	255	97
-	-403	-11087	2040	-732	-1329	-757	-1293	*	*											
195	2641	-824	2257	-2419	-1008	-709	-202	-1527	-1192	-522	-3524	-840	423	-426	716	-420	1047	762	1520	1028
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	255	97
-	-17	11046	-6446	-732	-1329	-731	-1332	*	*											
196	-1816	635	2060	-1451	-76	334	-236	-1681	-1280	-1333	-3786	-3273	-1083	-3182	-692	428	36	3121	3354	2987
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	-255	-97
-	-27	-11339	-5768	-732	-1329	-1959	-429	*	*											
197	-2888	900	-323	-914	1001	-844	-566	-2822	-2656	-856	-3771	-3258	-51	-3167	-730	168	-1471	-2522	3798	3235
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11322	-12322	-732	-1329	-1831	-476	*	*											
198	-1467	36	-1485	-602	-146	-149	-363	-2288	-1161	-545	-3796	-3284	-1346	-3192	-1694	-463	1868	-357	3940	1964
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-23	-11350	-6024	-732	-1329	-2468	-288	*	*											
199	-1500	902	-1452	-912	-1136	-583	-1543	-784	-878	-896	-2103	-1282	-1313	-1131	-14	-506	2289	-1171	-3352	2818
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11325	-12325	-732	-1329	-2587	-263	*	*											
200	-2892	-2118	-3276	-863	-590	-405	-968	-3733	-1350	-5	-282	-3262	1458	-635	-322	-154	410	-163	274	3197
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11325	-12325	-732	-1329	-2006	-413	*	*											
201	-1282	36	-2042	-65	-3155	1633	153	-3755	-1381	-688	-1360	-955	2283	-1759	-3454	-1164	1062	-196	-3374	699
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-49	-11350	4915	-732	-1329	-2468	-288	*	*											
202	-2872	59	-1263	-1690	-3114	2205	-2493	-1663	-1353	-949	-3754	-1291	599	-3151	-3413	1382	1217	-894	2039	-3174
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11304	12304	732	-1329	-3113	-177	*	*											
203	-2872	888	-3256	-924	448	-182	-340	-331	-2640	949	-3754	-3242	546	-3151	-3413	2179	242	-894	258	-890
	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

-	-1	-11304	-12304	-732	-1329	-1341	-725	*	*										
204	2456	36	1485	-1052	-1757	-2747	1558	-3755	-1381	1725	3796	-1315	526	-3192	-1092	428	2179	196	238	3216
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	73	-335	54	27	-12	255	-97
-	-1	-11350	12350	-732	-1329	2468	-288	*	*											
205	-2109	1801	-2537	10	119	-2747	2056	-2842	-2681	-129	-3796	-2432	215	-3192	-3454	-363	2839	769	238	3216
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-	-1	-11350	12350	-732	-1329	2468	-288	*	*											
206	-1467	1391	-3298	-533	-1169	-1527	-1558	264	-1381	-888	-3796	-1315	2131	-1500	-742	-327	2552	-3131	-3374	-3216
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11350	12350	-732	-1329	-2468	-288	*	*											
207	-1467	726	-549	144	-3155	-2296	-363	-1687	-1380	-1339	-3796	-554	3250	-3192	-1498	-1040	37	444	238	-3216
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11350	-12350	-732	-1329	-2468	-288	*	*											
208	-2456	1720	-1225	-77	-1169	-822	424	-1687	-1381	593	-628	-901	2878	-1164	-697	-894	-669	-917	238	-3216
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-	-7	-11350	-7857	-732	-1329	-2468	-288	*	*											
209	-470	2735	-1221	-331	-2286	-1524	601	451	-2676	1642	-3791	-3278	703	-3187	-3449	85	-1044	-915	1744	223
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-11344	-12344	-732	-1329	-2172	-362	*	*											
210	-561	1625	-1137	1462	-3155	-2747	-1558	-870	-2681	1292	-3796	-1434	-581	519	-2610	485	755	-145	1178	-3216
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-	-1	-11350	-12350	-732	-1329	-2468	-288	*	*											
211	-1024	2344	-76	2229	-1169	-2296	-2534	-707	-1161	-655	-628	-1900	-1346	-1164	-1498	611	-612	149	2406	-3216
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-	-1	-11350	-12350	-732	-1329	-2468	-288	*	*											
212	-789	3312	-3298	100	-3155	197	1213	386	-1161	-102	-3796	-622	-3079	-1164	-1002	-528	7	1498	238	-3216
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-	-1	-11350	-12350	-732	-1329	-2468	-288	*	*											
213	-1680	867	-1485	-447	-3155	-876	632	631	-1381	-1113	-3796	-3284	-1346	-1164	-343	-1744	1222	2541	1023	-3216
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-	-1	-11350	-12350	-732	-1329	-2468	-288	*	*											
214	-1680	-2140	14	-67	103	-1527	355	-981	-438	-719	-628	-2432	-1346	-1164	-1498	-1314	1983	472	4022	-3216
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-	-1	-11350	-12350	-732	-1329	-2468	-288	*	*											
215	-2913	36	-1485	-295	-2293	-2747	-250	1413	-251	-914	289	-1315	285	422	-1498	-1040	-350	-209	4550	-3216
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-	-1	-11350	-12350	-732	-1329	-2468	-288	*	*											
216	-2913	867	-1485	-1930	-364	-2747	594	2568	-708	-914	-628	-3284	-581	-353	-697	-1744	282	1306	1990	-3216
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-	-1	-11350	-12350	-732	-1329	-2468	-288	*	*											
217	-266	1787	-707	-3471	280	-1527	1075	183	-2681	878	-3796	-3284	-169	-891	-1616	-570	-764	2191	-3374	-3216
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-	-23	-11350	-6024	-732	-1329	-2468	-288	*	*											
218	-470	-2118	-1568	-3450	997	-2725	-53	-957	1360	1157	1508	-1116	374	115	-5	-535	-2438	594	-3352	-2140
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-	-1	-11325	-12325	-732	-1329	-2587	-263	*	*											
219	-510	-2118	-1369	1306	1154	-1497	-2512	-316	1915	-854	-1349	-177	-1426	-862	-196	104	532	-1604	-3352	-2140
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-	-1	-11325	-12325	-732	-1329	-2587	-263	*	*											
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221	-1595	-2140	-3298	268	-1757	-2296	-363	1672	-619	-463	359	-1315	2338	715	-634	18	-29	-1541	3374	-2154
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	-23	-11350	-6024	732	-1329	2468	-288	*	*											
222	-2438	-1145	-2521	-1430	-329	-2725	-2512	1865	-719	-864	498	-379	488	1318	-363	1194	560	30	-3352	-2140
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223	-441	-2118	-256	-1601	-2277	-1497	-1543	500	-372	-302	-3774	-1017	-663	-159	255	1800	-966	1568	-3352	-3194
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	-24	-11325	-5982	-732	-1329	-2587	-263	*	*											
224	-1617	-2096	-3253	-876	95	-1260	764	550	-701	105	-556	-1248	-982	830	-3410	1439	-873	1745	-3330	-931
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	-1	-11299	-12299	-732	-1329	-2696	-242	*	*											
225	-1231	-2096	-2505	-1497	-3111	-2703	32	-1298	-920	36	219	-987	-779	346	-472	2616	-607	-1411	311	797
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-24	-11299	-5939	-732	-1329	-2696	-242	*	*											
226	-1538	-2072	832	1348	814	-2679	-259	-3687	-1048	-684	-3728	-1212	-971	1043	48	1909	-1170	-2082	-3306	-305
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	-7	11272	-7829	-732	-1329	-2221	-348	*	*											
227	305	-2091	-351	1627	-1099	-1036	-221	-3705	-291	-660	-247	-2394	-509	2358	-111	242	-1644	-805	-3325	-502
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	-31	-11294	-5607	-732	-1329	-2786	-226	*	*											
228	-1578	146	-3220	-337	-1060	-1426	278	-2234	-139	878	1511	-3206	-1239	3002	-584	-101	-3015	-494	-3296	-802
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229	358	197	-594	-428	570	-2228	-2456	-1056	-184	582	-2064	-3206	-1239	1494	239	19	-3015	1532	961	3138
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230	-1313	-2027	2444	1093	-3043	-2635	83	-2753	1373	1815	-3	784	-425	733	-540	182	-654	-1489	-455	3103
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231	-623	189	1089	788	2147	-725	625	-3642	1764	437	-3683	-3171	-2966	-3079	-237	-1379	-748	211	-1262	-3103
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	-52	-11222	-4845	-732	-1329	-3182	-168	*	*											
232	-679	-1975	-3133	1254	2691	-646	-2369	-3589	-477	-167	-3631	172	-2914	-3027	1977	-264	-85	-139	-1237	-213
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-52	-11161	4849	-732	-1329	-2453	-291	*	*											
233	-72	257	-3116	-705	113	504	-2353	-3573	-359	-630	-79	-430	-1098	-1635	2266	1416	47	-2950	-3192	-3034
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	-85	-11142	4134	-732	-1329	-2991	-194	*	*											
234	-571	428	-3030	771	-2887	-2479	-1368	-3486	1724	1507	-1958	-183	-966	-1211	-368	262	-1247	-890	-3106	409
	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-32	-11037	5530	-732	-1329	-2519	-277	*	*											
235	-493	275	-273	283	-66	-1212	-2298	-3519	347	1911	-3560	942	-232	-1609	-2434	-292	-1173	-678	-3138	-706
	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-75	-11076	4320	-732	-1329	-3463	-137	*	*											
236	-366	344	-833	-627	1233	-1114	-2222	-357	-781	-191	-1926	2291	-910	-2880	-1508	770	-536	334	-3062	-25
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-8	-10985	-7703	-732	-1329	-2386	-306	*	*											
237	-1376	364	-3065	-613	2432	-150	878	-1120	-1075	-516	1007	1502	-2846	-2959	-361	521	389	-1324	-3141	-397
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-116	-11081	-3708	-732	-1329	-2142	-371	*	*											
238	417	-1876	1189	-99	-2891	66	543	-3491	-578	-715	1189	2446	-232	-959	-3190	-609	33	67	596	263

-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-31	-11047	-5589	-732	-1329	-2551	-270	*	*	*	*	*	*	*	*	*	*	*	*	*
239	-1639	-1912	339	1557	2927	1714	1171	-3527	847	-1727	-165	691	-1065	-415	-1897	-621	-212	-950	-3146	-2988
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-	-40	-11090	-5231	-732	-1329	-2114	-379	*	*	*	*	*	*	*	*	*	*	*	*	*
240	-1657	-1913	171	2040	862	926	-822	-3527	-1131	-1537	-3569	1257	236	549	-134	47	-1204	-607	-3147	-2989
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-	-83	-11089	-4166	-732	-1329	2358	-313	*	*	*	*	*	*	*	*	*	*	*	*	*
241	-2	793	81	1349	-861	1888	-2295	-3515	-2442	-2569	-307	1023	-266	349	-1190	-613	-2853	-170	562	-1962
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-	-111	-11076	-3763	-732	-1329	-2107	-381	*	*	*	*	*	*	*	*	*	*	*	*	*
242	-1050	270	102	1918	-2924	-1215	821	-3523	-333	-1765	-393	943	1405	481	405	-2390	-817	317	-3143	-2985
-	94	-11091	-3997	-732	-1329	-3646	-120	*	*	*	*	*	*	*	*	*	*	*	*	*
243	-2149	337	296	1325	-1985	-2442	-1250	-3449	-1227	-1038	-328	-50	2802	-863	-927	-537	-2148	11	538	-220
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     -   -3259   -161  -9859    -58  -4658  -4637    -59  -5111      *
     2     123   -338    248   1776  -1353    523    869  -1953    251  -1448   -532  -1482    497  -1158  -1652    376   -257  -1133  -1572    228
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-	-69	-9725	-4461	-732	-1329	-4450	-68	*	*										
30	636	-751	-512	97	198	187	-1145	-2365	-97	-414	629	-190	403	-68	-1425	477	984	118	-1985	-1827
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-145	-9657	-3401	-732	-1329	-3642	-120	*	*										
31	578	-700	-1411	514	-1342	638	-1094	1053	-1040	-462	-2355	-315	-1638	-25	-568	336	658	40	-1934	106
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-42	-9587	-5173	-732	-1329	-3125	-176	*	*										
32	-1286	-775	-159	94	-883	339	677	671	-205	342	-1957	-1206	-1714	1310	12	-701	553	-478	-2009	1069
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-	-3	-9691	-10691	-732	-1329	-4397	-70	*	*										
33	437	-775	793	-55	-1791	732	-1170	258	-772	324	336	523	-1714	-1541	164	89	-105	-413	-2009	-1041
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-	-3	-9691	-10691	-732	-1329	-4397	-70	*	*										
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9691	-10691	-732	-1329	-4397	-70	*	*										
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9691	-10691	-732	-1329	-3813	-107	*	*										
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9728	-10728	-732	-1329	-4248	-78	*	*										
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-	-18	-9728	-6438	-732	-1329	-3886	-101	*	*										
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-	-49	-9732	-4964	-732	-1329	-3907	-100	*	*										
39	-307	-783	458	-1517	-1799	-1341	-2	558	-498	705	-425	517	669	504	230	-250	-300	-261	-2017	671

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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-13	-9705	-7013	-732	-1329	-3668	-118	*	*											
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-	-78	-9738	-4286	-732	-1329	-4247	-78	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-194	-9661	-3003	-732	-1329	-3478	-136	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	-61	-9679	-4629	-732	-1329	-3690	-116	*	*											
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47	-553	-770	-687	-490	-1464	-1282	1037	796	-900	-382	-1748	233	393	1380	-1037	-730	338	1258	-1456	208
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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49	-96	-793	1036	-666	-112	-1381	431	-1079	-250	-1178	357	934	-1198	-594	98	-383	386	1436	-2028	-187
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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50	-530	-796	-1474	-158	-632	-397	-306	143	-451	117	-1431	1265	-430	-345	-963	-124	210	1212	-1882	858
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-	-16	-9720	-6619	-732	-1329	-3672	-118	*	*											
51	-733	-807	872	151	-609	-831	-1202	-512	-1085	174	-1417	315	265	-118	588	-1327	680	830	-2042	-1883
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	-3	-9749	-10749	-732	-1329	-4103	-87	*	*											
53	-55	947	236	380	-588	-389	-213	41	-361	-540	-323	1115	219	-174	-711	-495	662	403	-2052	-1894
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54	159	-751	289	572	77	-55	-1145	105	-1292	-296	-2407	774	1059	-615	-509	-669	-481	876	-1985	-1827
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59	12	-553	1111	-1011	-1	-252	-764	-1203	189	-1388	-916	989	1288	-411	-829	-619	692	-192	-1787	458
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61	233	-449	-245	433	1122	-969	54	-1251	-306	-638	-1112	819	-494	209	-89	-209	820	177	-1338	-302
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63	-577	714	-1482	-842	-821	-986	87	297	561	-105	-2035	867	371	-1431	-849	-558	973	1284	-1613	-652
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65	-379	-251	636	-1582	607	-858	-645	882	-303	-303	-1907	59	65	-1303	-938	-636	-208	1745	-1485	-1327
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67	-353	-27	1175	-1514	276	-790	-577	958	125	110	-1839	-1327	632	-1235	-1497	-567	-137	1162	-1417	-1259
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68	-879	-136	740	-234	146	-743	668	128	-154	83	-1791	949	696	-126	-1055	-1115	348	666	-1370	-1212
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69	-506	-136	1261	-117	-76	-440	-530	9	177	-616	-1313	614	336	-58	-1450	-1169	-1088	1457	-1370	-1212
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-	-162	-8506	-3271	-732	-1329	-5497	-32	*	*										
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74	-33	71	1534	73	-944	-536	806	-1282	188	-1039	-1585	732	1809	-981	-244	-962	-882	-921	-1163	-1005
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76	407	179	-935	384	1376	-401	-215	-1380	499	-446	-1477	-965	1226	2	-232	155	-329	-768	-1055	-897
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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77	-457	316	-841	-1015	1901	-291	-78	-1298	-225	-793	-1339	-827	2057	-736	-998	-717	472	26	-918	-759
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-	-438	-7805	-1957	-732	-1329	-5702	-28	*	*										
78	-281	492	-665	-171	1368	-115	98	-956	804	-352	-1164	-651	-446	818	81	-541	-149	240	970	-584
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-	-522	-7424	-1749	-732	-1329	-5819	-26	*	*										
79	-107	666	-492	-665	2478	59	272	-948	125	-443	-990	-477	-272	-386	-648	-367	-286	-325	-568	-410
-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
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RF    no
CS    no
COM   [converted from an old Plan9 HMM]
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DATE  Mon Mar  8 11:43:15 1999
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NULT      -4  -8455
NULE     595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM        A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y

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        -5111      *    -42
    1     -70   -217     41   -121  -1232   -394   -611    624   -387  -1326  -1873    158   2390  -1269   -105  -1250    -90    -33  -1451  -1293
    -     206    979   -179   -352    -35    372    585   -632    437   -131   -677   -164     41    -73   -335    -54     26    -12   -255    -96
    -   -3259   -161  -9859    -58  -4658  -4637    -59  -5111      *
    2     123   -338    248   1776  -1353    523    869  -1953    251  -1448   -532  -1482    497  -1158  -1652    376   -257  -1133  -1572    228
    -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
    -      -4  -9055 -10055   -732  -1329  -5201    -40      *      *
    3     294   -360    298  -1692   -201    823   -755  -1975   -830    -51  -2016   1103   -187    440   -374   -437  -1313   1364  -1594  -1436
    -     206    979   -179   -352    -36    372    585   -634    438   -130   -675   -164     41    -73   -332    -54     26    -12   -254    -97
    -   -3490   -136 -10090    -53  -4802  -4526    -64      *      *
    4    -510   -433    736  -1764    369   -300   -827   1707   -783   -493  -2088   -690   1083   -581    175  -1466   -126     55  -1667.    488
    -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
    -     -60  -9201  -4681   -732  -1329  -5513    -32      *      *
    5   -1108   -395  -1552  -1726    -75   -175   -789    216   1610   -834  -2051   1159  -1333   -678   -879    850    874   -493  -1629    197
    -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
    -      -4  -9143 -10143   -732  -1329  -4603    -61      *      *
    6    -205   -454   -485  -1786    862   1057    238    769   -996  -1564    640   -432   -859  -1506   -497   -826    422   1404      6  -1343
    -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
    -      -4  -9234 -10234   -732  -1329  -4719    -56      *      *
    7   -1276   -503    134  -1834    299   -226   -812    126  -1044    995  -2158    601   1587  -1555   -709   -716    280    169  -1737   -428
    -     205    979   -176   -353    -36    372    585   -634    438   -131   -677   -164     41    -73   -335    -54     27    -12   -255    -96
    -   -3707   -116 -10307    -46  -4980  -5467    -33      *      *
    8    -359   -475   1207    221  -1129  -1082    397    524   -826   -275    710  -1618  -1414   -779   -469   -333    201   1530  -1709  -1551
    -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
    -      -4  -9265 -10265   -732  -1329  -4429    -69      *      *
    9     -20   -542    726   -528     41    643   -937  -2157  -1084  -1211    794   2032   -167    -34   -440  -1098    604   -277  -1776  -1142
    -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
    -      -3  -9365 -10365   -732  -1329  -5443    -34      *      *
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10	-598	-542	1430	-1874	-182	261	-511	-2073	282	-372	-777	1149	499	371	-1856	-1003	529	317	-1776	19
-	206	979	-178	-352	-36	372	585	-635	438	-131	-677	-161	40	-73	-335	-54	27	-12	-255	-97
-	-3765	-111	-10365	-42	-5127	-4964	-47	*	*											
11	-1295	-597	-73	-1929	-1612	632	-200	1248	-589	-1102	-143	-1083	180	-55	-280	1788	141	-1460	-1831	-1291
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9444	-10444	-732	-1329	-4495	-65	*	*											
12	-1176	-647	1193	-1979	1026	178	-1041	725	-1	-1757	-2303	-508	1857	211	-788	-945	-349	-57	-1881	-357
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9515	-10515	-732	-1329	-5160	-41	*	*											
13	-821	-656	360	1728	81	-911	-173	260	-326	-1766	-2312	-1491	-717	333	857	-69	852	-829	-1890	-798
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-51	-9527	-4914	-732	-1329	-4925	-48	*	*											
14	-144	-641	-761	-1973	1696	-335	410	1135	-486	-1413	-785	-1785	302	-1618	228	-395	674	363	-1876	879
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-256	-9507	-2632	-732	-1329	-4097	-87	*	*											
15	380	-541	1053	-992	735	-221	-8	352	-991	-1044	-1868	-306	320	-1398	156	217	1171	-1398	-1775	-8
-	206	979	-179	-352	-36	372	585	-635	437	-130	-676	-164	41	-73	-335	-54	28	-12	-255	-96
-	-3733	-114	-10372	-43	-5104	-4898	-49	*	*											
16	-1243	-569	-300	-124	251	-97	991	381	419	228	394	-1036	-536	-944	-281	-814	980	241	578	106
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9410	-10410	-732	-1329	-5136	-42	*	*											
17	-22	-581	806	-1860	475	-1188	-293	391	-869	-63	-2237	882	-1520	-6	-362	981	530	-635	-1815	493
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9427	-10427	-732	-1329	-4718	-56	*	*											
18	-396	-598	-209	249	-1613	677	-279	-165	257	211	-50	-1742	-133	-783	1382	-655	333	57	-1832	-1674
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-	-10	-9449	-7518	-732	-1329	-4497	-65	*	*											
19	-385	-634	1013	594	312	279	-651	617	-181	14	-2290	56	-720	-289	-333	-1602	492	-223	-146	-785
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9501	-10501	-732	-1329	-5142	-41	*	*											
20	-768	-639	1117	-899	-1654	-115	-1033	812	726	-676	-1546	808	297	-894	644	203	-95	-354	-1873	-1715
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9507	-10507	-732	-1329	-4717	-56	*	.*											
21	-225	-654	-487	271	-139	-304	652	335	-189	-1763	-2309	288	419	-830	1052	538	-1044	901	-1888	-878
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-39	-9526	-5289	-732	-1329	-4526	-64	*	*											
22	-537	-657	-157	1082	648	-998	-354	-481	770	-194	-2190	158	437	674	-1388	-775	897	-473	-1891	-1665
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-81	-9531	-4236	-732	-1329	-4117	-86	*	*											
23	-936	-661	5	-1422	409	-608	252	-363	29	-92	-796	403	900	1083	25	-28	559	55	-128	-953
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-104	-9537	-3874	-732	-1329	-3502	-133	*	*											
24	-736	46	379	267	950	296	279	424	572	-331	-2331	-159	-1371	934	561	-829	-986	-57	-1909	-1751
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

-	-3	-9553	-10553	-732	-1329	-3494	-134	*	*										
25	-862	-765	757	-103	407	-276	-615	-630	-57	-482	-647	33	252	339	680	-571	733	-52	-1999	641
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-50	-9677	-4930	-732	-1329	-3921	-99	*	*										
26	-1526	-753	-143	400	1231	-204	1618	1162	-1294	411	-1739	-518	-751	-121	-684	-458	260	-516	566	-1828
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-129	-9660	-3563	-732	-1329	-3973	-95	*	*										
27	-794	-696	1540	423	-1711	-976	-492	480	-67	397	-870	-143	-219	-111	336	-384	-792	-940	-1930	899
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9581	-10581	-732	-1329	-3282	-157	*	*										
28	-731	-801	288	-5	-1064	-558	143	1436	-1207	-1104	-640	202	-51	-901	528	-82	1001	-271	-2035	671
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9725	-10725	-732	-1329	-4450	-68	*	*										
29	-777	-801	182	1268	-173	-178	-1147	302	651	-540	-2456	651	-910	-1853	598	-633	490	78	-2035	-1877
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-69	-9725	-4461	-732	-1329	-4450	-68	*	*										
30	636	-751	-512	97	198	187	-1145	-2365	-97	-414	629	-190	403	-68	-1425	477	984	118	-1985	-1827
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-145	-9657	-3401	-732	-1329	-3642	-120	*	*										
31	578	-700	-1411	514	-1342	638	-1094	1053	-1040	-462	-2355	-315	-1638	-25	-568	336	658	40	-1934	106
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-42	-9587	-5173	-732	-1329	-3125	-176	*	*										
32	-1286	-775	-159	94	-883	339	677	671	-205	342	-1957	-1206	-1714	1310	12	-701	553	-478	-2009	1069
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9691	-10691	-732	-1329	-4397	-70	*	*										
33	437	-775	793	-55	-1791	732	-1170	258	-772	324	336	523	-1714	-1541	164	89	-105	-413	-2009	-1041
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9691	-10691	-732	-1329	-4397	-70	*	*										
34	-1082	-775	12	-38	-1153	-1155	-345	38	481	362	353	-1097	-127	279	491	210	676	321	-1480	-14
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9691	-10691	-732	-1329	-4397	-70	*	*										
35	-96	-775	224	40	-1514	-210	-1170	370	-82	-216	-37	141	-1714	-342	-258	-133	773	586	-1830	1130
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9691	-10691	-732	-1329	-3813	-107	*	*										
36	208	-803	-718	-1535	-1192	-1260	-439	38	548	-315	-250	534	-205	-838	333	-82	380	707	872	1268
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9728	-10728	-732	-1329	-4248	-78	*	*										
37	369	-803	-897	893	-1167	-244	403	332	-314	577	-2458	-384	693	-740	-471	-1126	207	476	-2037	-1878
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-	-18	-9728	-6438	-732	-1329	-3886	-101	*	*										
38	391	-806	169	-1716	-103	-229	-1200	-1149	7	588	219	953	631	414	-668	-377	558	-532	-2040	-1158
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-49	-9732	-4964	-732	-1329	-3907	-100	*	*										
39	-307	-783	458	-1517	-1799	-1341	-2	558	-498	705	-425	517	669	504	230	-250	-300	-261	-2017	671

-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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40	50	-786	1003	109	-1801	-426	54	240	-651	-53	-2442	-1008	236	-1838	1520	304	-1323	429	-2020	-1862
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-13	-9705	-7013	-732	-1329	-3668	-118	*	*											
41	183	-810	-742	1011	-731	334	-404	-928	-942	650	-2466	-642	-1206	-122	903	-1843	-285	583	-181	518
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-78	-9738	-4286	-732	-1329	-4247	-78	*	*											
42	-75	-754	1094	476	-1769	-500	-203	-21	-1295	-1814	-2410	427	-511	228	853	818	591	-36	-1988	-1830
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-194	-9661	-3003	-732	-1329	-3478	-136	*	*											
43	681	-676	620	490	-1319	-627	-137	-1627	-250	-137	-1056	313	-38	-201	1005	-896	516	-721	-1910	505
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-77	-9553	-4305	-732	-1329	-2989	-194	*	*											
44	210	-763	-892	983	-1778	77	-1157	1046	-1125	-662	-412	790	-771	984	-485	-971	87	601	-1997	-1839
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-80	-9675	-4254	-732	-1329	-3369	-147	*	*											
45	-219	-766	-596	135	-652	397	-803	1168	208	-647	-2422	143	-2	-56	2	-371	871	-475	927	-1842
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-61	-9679	-4629	-732	-1329	-3690	-116	*	*											
46	-545	-192	468	-562	-1470	344	995	-2038	-1190	154	942	23	-1466	881	-83	-576	387	968	-489	118
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-	-42	-9663	-5177	-732	-1329	-3620	-122	*	*											
47	-553	-770	-687	-490	-1464	-1282	1037	796	-900	-382	-1748	233	393	1380	-1037	-730	338	1258	-1456	208
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-11	-9685	-7306	-732	-1329	-3640	-121	*	*											
48	-249	-801	1173	215	-935	-507	402	-244	-1342	366	-2334	706	343	-6	-2065	-750	-192	452	-1819	975
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-19	-9727	-6352	-732	-1329	-4033	-91	*	*											
49	-96	-793	1036	-666	-112	-1381	431	-1079	-250	-1178	357	934	-1198	-594	98	-383	386	1436	-2028	-187
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-20	-9716	-6290	-732	-1329	-3835	-105	*	*											
50	-530	-796	-1474	-158	-632	-397	-306	143	-451	117	-1431	1265	-430	-345	-963	-124	210	1212	-1882	858
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-16	-9720	-6619	-732	-1329	-3672	-118	*	*											
51	-733	-807	872	151	-609	-831	-1202	512	-1085	174	-1417	315	265	-118	588	-1327	680	830	-2042	-1883
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9735	-10735	-732	-1329	-3920	-99	*	*											
52	-289	137	440	-429	-1245	-1425	-1212	1239	-34	265	-569	396	369	-659	-16	-1851	-269	953	-2052	-89
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9749	-10749	-732	-1329	-4103	-87	*	*											
53	-55	947	236	380	-588	-389	-213	41	-361	-540	-323	1115	219	-174	-711	-495	662	403	-2052	-1894
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-92	-9749	-4041	-732	-1329	-4103	-87	*	*											

54	159	-751	289	572	77	-55	-1145	105	-1292	-296	-2407	774	1059	-615	-509	-669	-481	876	-1985	-1827
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-64	-9658	-4566	-732	-1329	-4532	-64	*	*											
55	-100	-705	-318	-214	-883	-598	-538	263	-101	33	-907	1116	922	-114	-334	25	135	404	-1939	-1530
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-35	-9595	-5473	-732	-1329	-4636	-59	*	*											
56	381	44	1665	302	216	-653	-941	-1411	74	-621	-1801	887	-678	-512	-1461	-755	766	80	-1916	-1758
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-89	-9562	-4092	-732	-1329	-4716	-56	*	*											
57	-172	-619	1279	-377	186	-1077	-1014	3	-313	-1034	-1877	1066	480	-330	-381	-345	649	640	-1854	-1695
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-113	-9474	-3759	-732	-1329	-4259	-77	*	*											
58	124	-583	405	-1093	-1552	109	-977	109	563	-1050	-2238	2002	686	-1084	-756	-523	-53	121	-1817	-897
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-45	-9421	-5099	-732	-1329	-4991	-46	*	*											
59	12	-553	1111	-1011	-1	-252	-764	-1203	189	-1388	-916	989	1288	-411	-829	-619	692	-192	-1787	458
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-54	-9379	-4829	-732	-1329	-4725	-56	*	*											
60	-391	-531	230	-158	63	80	360	691	-984	-484	-2187	1022	1232	-1090	-1776	-602	518	426	-1765	-1607
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-122	-9346	-3652	-732	-1329	-5120	-42	*	*											
61	233	-449	-245	433	1122	-969	54	-1251	-306	-638	-1112	819	-494	209	-89	-209	820	177	-1338	-302
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-105	-9225	-3861	-732	-1329	-4698	-57	*	*											
62	-542	-412	886	26	304	-988	-806	-196	-483	-446	978	-1275	1877	-515	-1349	270	-653	185	-1646	-841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-81	-9169	-4247	-732	-1329	-4674	-58	*	*											
63	-577	714	-1482	-842	-821	-986	87	297	561	-105	-2035	867	371	-1431	-849	-558	973	1284	-1613	-652
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-30	-9118	-5732	-732	-1329	-5214	-39	*	*											
64	-218	-362	591	-710	1123	-969	-537	305	940	-59	-2017	894	-823	-248	532	-818	-630	-89	-456	-1110
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-175	-9090	-3155	-732	-1329	-5239	-39	*	*											
65	-379	-251	636	-1582	607	-858	-645	882	-303	-303	-1907	59	65	-1303	-938	-636	-208	1745	-1485	-1327
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-113	-8912	-3777	-732	-1329	-5382	-35	*	*											
66	-886	-183	-1213	-221	-647	-790	-161	-915	239	352	-1839	1571	-1122	594	683	-954	492	727	-1417	-444
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8801	-9801	-732	-1329	-5421	-34	*	*											
67	-353	-27	1175	-1514	276	-790	-577	958	125	110	-1839	-1327	632	-1235	-1497	-567	-137	1162	-1417	-1259
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-82	-8801	-4232	-732	-1329	-5421	-34	*	*											
68	-879	-136	740	-234	146	-743	668	128	-154	83	-1791	949	696	-126	-1055	-1115	348	666	-1370	-1212
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

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-     -5  -8719  -9719   -732  -1329  -5443    -34      *      *
69  -506   -136   1261   -117    -76   -440    -530      9    177   -616  -1313    614    336    -58  -1450  -1169  -1088   1457  -1370  -1212
-   206    979   -178   -352    -36    372     585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
-  -109  -8719  -3824   -732  -1329  -5443    -34      *      *
70    38    -73   1252   -672    468   -406     133   -263   -592   -671  -1149    974    677   -979  -1388   -279     72    670  -1308  -1149
-   206    979   -178   -352    -36    372     585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
-  -103  -8610  -3914   -732  -1329  -5476    -33      *      *
71  -790    -17   2062   -696  -1032   -624    -411   -867   -558  -1126  -1673   2130   -956  -1069    292  -1050   -970    388  -1251  -1093
-   206    979   -178   -352    -36    372     585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
-    -6  -8506  -9506   -732  -1329  -5497    -32      *      *
72   175    -17   1314   -452    913   -624    -411   -179   -325  -1066  -1673   1683    218    137  -1331   -677   -204   -418  -1251  -1093
-   206    979   -178   -352    -36    372     585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
-  -162  -8506  -3271   -732  -1329  -5497    -32      *      *
73  -379     71    849   -780   -675   -536      -5  -1544   -471   -553  -1585   2472   1258   -981  -1058   -241   -882   -921  -1163  -1005
-   206    979   -178   -352    -36    372     585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
-    -7  -8338  -9338   -732  -1329  -5530    -32      *      *
74   -33     71   1534     73   -944   -536     806  -1282    188  -1039  -1585    732   1809   -981   -244   -962   -882   -921  -1163  -1005
-   206    979   -178   -352    -36    372     585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
-    -7  -8338  -9338   -732  -1329  -5530    -32      *      *
75  -331     71  -1087   -654    975    275     464   -801   -471  -1039  -1585   1561   1660   -328     58   -713   -132   -680  -1163  -1005
-   206    979   -178   -352    -36    372     585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
-  -216  -8338  -2878   -732  -1329  -5530    -32      *      *
76   407    179   -935    384   1376   -401    -215  -1380    499   -446  -1477   -965   1226      2   -232    155   -329   -768  -1055   -897
-   206    979   -178   -352    -36    372     585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
-  -304  -8119  -2422   -732  -1329  -5608    -30      *      *
77  -457    316   -841  -1015   1901   -291     -78  -1298   -225   -793  -1339   -827   2057   -736   -998   -717    472     26   -918   -759
-   206    979   -178   -352    -36    372     585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
-  -438  -7805  -1957   -732  -1329  -5702    -28      *      *
78  -281    492   -665   -171   1368   -115      98   -956    804   -352  -1164   -651   -446    818     81   -541   -149    240    970   -584
-   206    979   -178   -352    -36    372     585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
-  -522  -7424  -1749   -732  -1329  -5819    -26      *      *
79  -107    666   -492   -665   2478     59     272   -948    125   -443   -990   -477   -272   -386   -648   -367   -286   -325   -568   -410
-     *      *      *      *      *      *       *      *      *      *      *      *      *      *      *      *      *      *      *      *
-     *      *      *      *      *      *       *      *      0
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LENG  63
ALPH  Amino
RF    no
CS    no
COM   [converted from an old Plan9 HMM]
NSEQ  0
DATE  Mon Mar  8 11:43:32 1999
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NULT       -4  -8455
NULE      595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM         A       C       D       E       F       G       H       I       K       L       M       N       P       Q       R       S       T       V       W       Y

          m->m    m->i    m->d    i->m    i->i    d->m    d->d    b->m    m->e
         -2108       *    -381
      1   -750      23    1183    1324    -992    -584    2548   -1592     398    -334   -1633   -1121    -916    1235   -1291   -1010    -930    -969   -1211   -1053
      -    206     979    -178    -352     -36     372     585    -635     438    -130    -677    -164      41     -73    -335     -54      27     -12    -255     -97
      -     -6   -8487   -9487    -732   -1329   -3382    -146   -2108       *
      2   -750      23   -1135   -1308    -992    -584    -371   -1592     971    1557   -1633   -1121    -916    2302   -1291   -1010    -930    -969   -1211   -1053
      -    206     979    -179    -351     -36     372     585    -636     438    -130    -677    -164      40     -73    -335     -54      28     -12    -255     -97
      -  -2887    -212   -9487     -81   -4197   -1685    -538       *       *
      3   -993    -220     -76    1048   -1235    -827    -614   -1834    1812     343   -1875     397   -1158    1001     676   -1253   -1172   -1211   -1454   -1295
      -    206     979    -178    -352     -36     372     585    -635     438    -130    -677    -164      41     -73    -335     -54      27     -12    -255     -97
      -     -5   -8911   -9911    -732   -1329   -2684    -244       *       *
      4    910    -247    -394     993   -1262    -854    -641   -1861    1267     515   -1902   -1390   -1185    1683   -1561   -1280   -1199    -327   -1481   -1323
      -    206     979    -178    -352     -36     372     585    -635     438    -130    -677    -164      41     -73    -335     -54      27     -12    -255     -97
      -     -4   -8954   -9954    -732   -1329   -1412    -680       *       *
      5  -1190    -417    -178    1870   -1432   -1024    -811   -2031    -958    1137   -2073    -423   -1355    1086     -55   -1450   -1369     711   -1651   -1493
      -    206     979    -178    -352     -36     372     585    -635     438    -130    -677    -164      41     -73    -335     -54      27     -12    -255     -97
      -     -4   -9214  -10214    -732   -1329   -1228    -803       *       *
      6   -587    1916   -1694    -882   -1552   -1144    -931     364    1033   -1646     275   -1680   -1475    1923    -650    -585    1131     869   -1770   -1612
      -    206     979    -178    -352     -36     372     585    -635     438    -130    -677    -164      41     -73    -335     -54      27     -12    -255     -97
      -     -3   -9387  -10387    -732   -1329    -519   -1728       *       *
      7     95    -682   -1840    1868   -1697   -1289    1372   -2297    1672     290     214   -1826   -1621    -343    -257   -1029   -1635    -338   -1916   -1758
      -    206     979    -178    -352     -36     372     585    -635     438    -130    -677    -164      41     -73    -335     -54      27     -12    -255     -97
      -     -3   -9591  -10591    -732   -1329     -33   -5451       *       *
      8   1295    -765   -1923    -159   -1780   -1372   -1159   -2379    1375     363     522   -1908   -1704    1301     909      35   -1717    -715   -1999   -1841
      -    206     979    -178    -352     -36     372     585    -635     438    -130    -677    -164      41     -73    -335     -54      27     -12    -255     -97
      -     -3   -9703  -10703    -732   -1329     -76   -4293       *       *
      9    111    -765   -1923     792    -353   -1372   -1159   -1265    1243     613    1797    -437   -1704   -1817    -792    1110   -1717    -324   -1999   -1841
      -    206     979    -178    -352     -36     372     585    -635     438    -130    -677    -164      41     -73    -335     -54      27     -12    -255     -97
      <     -3   -9703  -10703    -732   -1329     -76   -4293       *       *
```

10	-97	-765	-1923	1931	-1780	-1372	-1159	-2379	889	-205	-2421	834	-1704	462	-2079	42	1031	-633	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*											
11	678	-765	-1923	1499	19	-1372	-1159	-1003	639	-1874	2448	155	-1704	-338	-1047	255	-862	-1756	-1999	926
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-	-134	-9703	-3516	-732	-1329	-76	-4293	*	*											
12	-210	-668	-1826	1622	-1683	-1275	-1062	-2283	985	966	-123	551	-1607	-1720	-1982	656	-1621	218	-1902	-1744
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9571	-10571	-732	-1329	-1349	-719	*	*											
13	206	-668	-1826	1035	-1683	-656	-1062	-2283	1500	-1777	-2324	1789	-1607	352	0	769	-299	-1659	-1902	-1744
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-67	-9571	-4507	-732	-1329	-1349	-719	*	*											
14	-400	-622	-1779	214	-1637	-1229	-1016	-2236	1435	18	-2277	1511	-1560	707	-1936	1176	-1574	566	-1856	-1698
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9507	-10507	-732	-1329	-371	-2140	*	*											
15	-1495	-722	191	1199	-1737	-1329	-1116	0	992	53	-2377	622	-1660	1106	-253	-268	276	167	-1956	-1798
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9645	-10645	-732	-1329	-805	-1226	*	*											
16	-334	-722	-1879	-2053	-1737	-1329	-1116	-1221	1902	722	-1115	1658	-1660	-460	355	219	-85	-931	-1956	-1798
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9645	-10645	-732	-1329	-45	-5022	*	*											
17	-95	-765	273	1474	-1780	-1372	-1159	-2379	-1306	-1874	-2421	93	-1704	2190	1291	296	346	-1756	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*											
18	-1538	1686	1504	-1195	-1780	-1372	-1159	-1003	178	1021	522	656	-1704	735	-2079	1006	-862	-1756	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*											
19	-702	-765	391	1171	-1780	-1372	-1159	-2379	353	1472	75	-437	-1704	1354	-2079	468	-1717	-1756	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*											
20	-1538	-765	1375	54	-1780	475	-1159	-2379	510	613	-2421	760	-1704	1066	343	580	-1525	-1756	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*											
21	501	-765	-699	623	-1780	-1372	-1159	-2379	211	1217	-2421	155	-1704	1550	-185	800	-1717	-1756	-1999	-1841
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-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*											
22	-305	-765	1108	1232	-1780	-1372	1076	476	-1306	-273	-2421	-126	-1704	986	842	509	-843	-1756	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*											
23	555	-765	-1923	1559	-1780	-1372	-1159	-40	-1306	884	-2421	1213	-1704	478	-460	-283	271	-1756	-1999	-1841
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-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*											
24	-1538	-765	1324	2246	-1780	56	269	-2379	-1306	-1874	-2421	324	-1704	547	-308	655	-564	-1756	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*										
25	-960	-765	1587	1219	471	-366	-1159	-2379	685	835	-2421	578	-1704	-563	-196	-1798	-1717	-633	-1999	-1841
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*										
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-	-3	-9703	-10703	-732	-1329	-76	-4293	*	*										
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-	-80	-9112	-4263	-732	-1329	-2511	-278	*	*											
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59	705	361	-797	326	-654	-246	-33	-920	-181	755	-1295	-783	-578	-691	-953	934	332	-631	-873	-715
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-	-449	-7247	-1937	-732	-1329	-3913	-99	*	*											
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-	-19	-6860	-7860	-732	-1329	-4022	-92	*	*											
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-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
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WO 00/63687 PCT/US00/10302

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DESC
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ALPH  Amino
RF    no
CS    no
COM   [converted from an old Plan9 HMM]
NSEQ  0
DATE  Mon Mar  8 11:40:16 1999
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NULT       -4  -8455
NULE      595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM         A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y

          m->m   m->i   m->d   i->m   i->i   d->m   d->d   b->m   m->e
          -202      *  -2939
      1    179    953   -205     84    -63    345    558   -662    411   -157   -703   -191     14   -100   -362    -81      0    -39   -282   -123
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -    -39  -5797  -6797   -732  -1329  -1611   -572   -202      *
      2    179    953   -205   -379    -63    345    558   -662    411   -157   -703   -191     14   -100   -362    -81    400    -39   -282   -123
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      -    -36  -5924  -6924   -732  -1329  -1478   -642      *      *
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
13	150	923	-234	-408	-92	316	529	-213	382	-186	-732	-220	-15	429	-391	-110	-29	78	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
14	150	923	-234	-408	-92	316	529	-691	382	-186	-732	763	-15	-129	-391	-110	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
15	150	923	-234	-408	-92	316	529	-691	382	-186	-732	-220	-15	512	-391	-110	-29	287	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
16	150	923	-234	-408	-92	316	529	-691	382	-186	-732	393	-15	-129	-391	223	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
17	150	923	-234	-408	-92	316	529	-691	382	-186	-732	-220	-15	429	-391	-110	-29	344	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
18	150	923	-234	-408	-92	316	529	-691	382	-186	-732	183	-15	-129	-391	355	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
19	150	923	-234	-408	-92	316	529	-691	382	91	-732	-220	-15	512	-391	-110	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
20	150	1546	-234	-408	-92	316	529	-691	382	-186	-732	-220	-15	-129	-391	277	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
21	150	923	-234	-408	-92	316	529	-691	382	137	-732	-220	-15	429	-391	-110	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
22	150	1637	-234	41	-92	316	529	-691	382	-186	-732	-220	-15	-129	-391	-110	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
23	150	923	236	-408	-92	316	529	-691	382	-186	-732	-220	-15	512	-391	-110	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*											
24	150	923	236	110	-92	316	529	-691	382	-186	-732	-220	-15	-129	-391	-110	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

WO 00/63687
PCT/US00/10302

-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*										
25	150	923	308	-408	-92	316	529	-691	382	-186	-732	-220	-15	-129	-391	-110	-29	-68	-311	529
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-36	-5924	-6924	-732	-1329	-1478	-642	*	*										
26	150	923	308	41	-92	316	529	-691	382	-186	-732	-220	-15	-129	-391	-110	-29	-68	-311	-152
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-165	-5924	-3451	-732	-1329	-1478	-642	*	*										
27	175	948	-210	-383	-67	341	554	-667	406	-162	-708	-196	9	-104	-366	-85	-5	-44	-286	668
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-39	-5810	-6810	-732	-1329	-1589	-583	*	*										
28	175	948	-210	147	-67	341	554	-667	406	-162	-708	-196	9	-104	-366	-85	-5	-44	-286	-128
-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
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CS    no
COM   [converted from an old Plan9 HMM]
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NULE      595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM         A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y

          m->m   m->i   m->d   i->m   i->i   d->m   d->b   b->m   m->e
          -552      *  -1653
      1   2062     13  -1144  -1318    244   -594   -381  -1601   1755  -1096  -1642  -1130   -925  -1039  -1301  -1020   -939   -177  -1221   -628
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -6  -8523  -9523   -732  -1329   -543  -1673   -552      *
      2   -780     -7   2178  -1338  -1022    180   -401  -1621   -548  -1116    954  -1150   -946   2132    467  -1040   -960   -998  -1241  -1083
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -6  -8558  -9558   -732  -1329   -630  -1499      *      *
      3   -780     -7  -1165  -1338  -1022   1560   -401  -1621   -275  -1116    954  -1150   -946  -1059   -197   1800   -960    353  -1241  -1083
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -6  -8558  -9558   -732  -1329   -630  -1499      *      *
      4   1737     -7  -1165  -1338  -1022   -614   -401  -1621   -548  -1116    954   2386   -946  -1059   -762  -1040   -128   -998  -1241  -1083
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -6  -8558  -9558   -732  -1329   -630  -1499      *      *
      5   -193   3780  -1165    259  -1022    277   -401  -1621   -548  -1116  -1663  -1150   -441  -1059  -1321   1412   -960   -998  -1241  -1083
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -6  -8558  -9558   -732  -1329   -412  -2010      *      *
      6   -797    -23  -1181   1916  -1039   -631   -418   -888   -565    269  -1679  -1167   1874   -401  -1338      5   -976  -1015  -1257  -1099
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -6  -8587  -9587   -732  -1329    -57  -4687      *      *
      7     73    -56   2129  -1388  -1071   -663   -451  -1671   -598    -44  -1712   1921   -995    323  -1370  -1090  -1009     -1  -1290  -1132
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -5  -8644  -9644   -732  -1329    -76  -4293      *      *
      8   -830    -56  -1214  -1388  -1071   -663   -451   -500   -598    -44   -363  -1200   2247   -324   -249  -1090  -1009   1721  -1290  -1132
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -    -646  -8644  -1480   -732  -1329    -76  -4293      *      *
      9   -491    283   -875  -1049   -733   -325   -112  -1332   -259    295   1953   -861   -656   2423  -1032   -751   -670    408   -951   -793
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -8  -8004  -9004   -732  -1329  -2034   -404      *      *
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10	411	283	2060	-1049	-733	-325	1883	-1332	103	-827	1710	-861	-656	-770	-1032	-751	-670	-709	-951	-793
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-763	-8004	-1298	-732	-1329	-2034	-404	*	*											
11	-182	591	-566	597	74	1526	197	-1023	50	-176	344	-552	-347	-461	-723	-442	-361	-400	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-7251	-8251	-732	-1329	-2653	-250	*	*											
12	924	591	-566	-740	-424	765	197	-1023	50	397	-1065	-552	-347	-461	-723	551	-361	-400	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-7251	-8251	-732	-1329	-2653	-250	*	*											
13	659	591	-566	858	-424	-16	197	-1023	50	397	-1065	219	-347	-461	-723	147	-361	-400	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-7251	-8251	-732	-1329	-2653	-250	*	*											
14	98	591	-566	-740	-424	-16	197	-1023	50	397	-1065	-552	1474	681	-85	-442	-108	-278	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-7251	-8251	-732	-1329	-2653	-250	*	*											
15	67	591	-566	-193	-424	-16	424	-1023	50	397	-1065	1248	-347	-294	-298	-442	-361	646	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-7251	-8251	-732	-1329	-2653	-250	*	*											
16	659	2591	-566	-740	-424	-16	1897	-79	50	-518	-1065	-552	-347	-461	-723	-442	-361	143	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-7251	-8251	-732	-1329	-2653	-250	*	*											
17	1345	591	-566	518	-424	874	197	-1023	50	-518	-1065	-552	-347	-461	-723	-442	-361	-400	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-7251	-8251	-732	-1329	-2653	-250	*	*											
18	769	591	1085	-278	-424	-16	197	-1023	50	481	-1065	-552	-347	-461	-83	-442	-361	-400	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-7251	-8251	-732	-1329	-2653	-250	*	*											
19	-182	591	-566	775	-424	-16	197	-1023	50	548	-1065	-552	1229	-461	-83	-442	-361	-400	-643	-485
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-376	-7251	-2166	-732	-1329	-2653	-250	*	*											
20	-67	707	-451	-625	-309	99	312	-908	165	948	-949	-437	1085	-345	-608	-327	-246	-285	-527	-369
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-18	-6891	-7891	-732	-1329	-2810	-222	*	*											
21	-67	707	-451	-625	-309	99	312	-908	165	948	-949	1084	-232	-345	-608	-327	-246	-285	-527	-369
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-18	-6891	-7891	-732	-1329	-2810	-222	*	*											
22	-67	2411	-451	-625	-309	99	1921	-908	432	168	-949	-246	-232	-345	-608	-327	-246	-285	-527	-369
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-18	-6891	-7891	-732	-1329	-2810	-222	*	*											
23	835	707	-451	-625	-309	929	948	-908	165	-403	-949	-437	-232	168	32	-327	-246	-285	-527	-117
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-18	-6891	-7891	-732	-1329	-2810	-222	*	*											
24	774	707	935	-625	-309	879	312	-908	165	-403	-949	-437	-232	-345	-608	-327	-246	-285	-527	-369
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

WO 00/69687

PCT/US00/10302

-	-18	-6891	-7891	-732	-1329	-2810	-222	*	*										
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-367	-6891	-2210	-732	-1329	-2810	-222	*	*										
26	27	800	-192	-71	-215	193	406	-815	259	-310	-856	302	1100	-252	-514	71	-153	-192	-434	-276
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-23	-6546	-7546	-732	-1329	-2921	-204	*	*										
27	27	800	-358	-531	-215	193	406	-815	259	-310	-856	1092	959	-252	-514	-119	-153	-192	-434	-276
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-23	-6546	-7546	-732	-1329	-2921	-204	*	*										
28	27	2413	26	-531	-215	193	406	-815	259	-310	-856	805	-139	-252	-514	-233	-153	-192	-434	-276
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-23	-6546	-7546	-732	-1329	-2921	-204	*	*										
29	867	1588	-358	-531	-215	193	406	-815	259	32	-856	-344	-139	-252	-514	-233	-153	133	-434	-276
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-23	-6546	-7546	-732	-1329	-2921	-204	*	*										
30	306	800	947	-374	-215	193	406	-815	619	-310	-856	-344	-139	261	-514	-233	-153	-192	-434	-276
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-23	-6546	-7546	-732	-1329	-2921	-204	*	*										
31	27	800	878	-531	-215	193	406	-815	259	-310	-856	-344	1100	-252	-514	-233	-153	-192	-434	-276
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-731	-6546	-1370	-732	-1329	-2921	-204	*	*										
32	171	944	-213	-387	-71	337	550	-670	403	-165	-712	-199	576	-108	-370	-89	-8	-47	-290	-132
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CS    no
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NULE      595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM         A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y

          m->m   m->i   m->d   i->m   i->m   d->m   d->d   b->m   m->e
         -1144      *   -869
     1    -501      7   -618  -1985    -97    281   -409   1925   -295    189  -1742  -1334  -1202    -56  -2169   -671   -701   1400  -1760  -1089
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -43 -12932  -5112   -732  -1329   -983  -1017  -1144      *
     2    -634   -614   -105   -796    760    727  -1553   1245    -25   -818  -2691   -843   -601  -1338   -123    -48   -593    855  -4869   1049
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -       0 -12944 -13944   -732  -1329   -357  -2191      *      *
     3    -341    820   -169  -2147  -1458    263  -1110   1629   -851   -362  -1805  -1355    -53   -507   -528   -622   -478   1758  -4942  -1259
     -     205    976   -178   -354    -39    374    583   -628    438   -133   -677   -163     37    -75   -333    -53     28     -8   -261    -94
     -   -7420    -13  -8263     -3  -8720  -1883   -456      *      *
     4    -150  -2770    410   -134   -623    715   -228    680     46   -580  -1079   -269   -679    111   -501    729  -2038    895  -4928  -1317
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -16 -13006  -6495   -732  -1329  -1039   -962      *      *
     5     260  -2763   -285   -935  -1072    383   -380   1383   -649   -111    693   -333    412    219   -682   -766  -2749   1203  -1858  -2122
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -16 -13004  -6516   -732  -1329  -1434   -667      *      *
     6     559  -2762    822   -321  -1370   1043   -259     16   -176    188    938   -502   -671    163   -411   -484   -783     43  -4920  -2754
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -33 -12997  -5463   -732  -1329   -615  -1527      *      *
     7     349  -1925    666     78  -3109    743    999   -381    120  -1005  -5338   -358   1253     98   -484   -219   -734    583  -4916  -4758
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -11 -12993  -7000   -732  -1329   -733  -1328      *      *
     8     350  -1175    306     -4  -1162   1723   -417    525   -745   -510  -3747    508     70    219   -566   -360  -1044   -883  -4932  -3211
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -18 -13009  -6311   -732  -1329  -1499   -630      *      *
     9     882    157    396   -424  -2651   1520   -542   -508   -802   -901  -1066  -1683    356   -110   -954    775   -773     -7  -1821  -2893
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -14 -12998  -6677   -732  -1329   -918  -1087      *      *
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10	1318	-1935	340	148	-1357	581	-1091	-86	-690	-381	-254	-57	1369	-368	-566	-247	-3102	-422	-1823	-3765
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-54	-13004	-4771	-732	-1329	-728	-1335	*	*											
11	1893	-639	-218	44	-1473	718	148	-311	-659	-351	-1770	-215	-1734	38	-854	-105	-1670	56	-1791	-4737
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-25	-12971	-5888	-732	-1329	-759	-1289	*	*											
12	978	-693	905	700	-2164	332	142	-44	-758	-383	-2272	-128	76	557	-1	-478	-2207	107	-1807	-1809
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-22	-12986	-6078	-732	-1329	-777	-1264	*	*											
13	805	-168	209	-366	-4699	557	-50	-935	937	26	-498	515	-2117	370	764	-839	-799	20	-4918	-2103
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-60	-12995	-4619	-732	-1329	-775	-1267	*	*											
14	584	275	1084	-322	-1250	1064	-664	-240	-295	-85	-466	-1322	-2121	402	5	358	-1242	19	-1786	-2505
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-60	-12961	-4611	-732	-1329	-473	-1839	*	*											
15	-1034	-624	386	-20	-2342	1988	33	367	-109	-199	162	-171	-1634	-588	307	-384	-1724	-119	-4884	-4726
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-128	-12960	-3565	-732	-1329	-510	-1747	*	*											
16	139	-963	1082	-542	-1824	244	-581	-344	134	129	-475	186	-984	354	1129	-268	-227	-31	-4815	-4657
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-22	-12888	-6063	-732	-1329	-541	-1677	*	*											
17	-350	-1679	-154	-190	-914	678	306	1357	-976	1179	118	-1391	-3267	140	-24	-1324	-587	164	-4922	-4764
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-21	-12999	-6119	-732	-1329	-831	-1191	*	*											
18	-506	83	276	282	-2197	318	1173	365	465	-288	-2944	-87	-1223	932	1004	-387	-1297	332	-4922	-3758
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-12998	-8242	-732	-1329	-440	-1927	*	*											
19	-27	-1188	830	-116	-946	277	152	639	136	-6	-124	347	288	-269	-161	-820	-1276	540	-931	-2932
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-11	-13024	-7032	-732	-1329	-1606	-575	*	*											
20	-295	-1604	963	369	-2488	1844	130	42	-506	-358	-859	-106	-1774	290	138	-1659	-1966	232	-1861	-3241
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-13013	-7268	-732	-1329	-1775	-499	*	*											
21	-155	-1092	2375	-419	-1908	-866	129	434	-1201	-111	-1287	96	-1285	-407	-572	-857	-918	776	-1827	-1650
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-2	-13005	-9614	-732	-1329	-747	-1307	*	*											
22	-218	-842	-151	-203	-3056	545	-256	881	-220	-8	-416	346	-2135	-143	634	-724	-637	1158	-375	-1555
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	0	-13022	-14022	-732	-1329	-1418	-676	*	*											
23	-64	-1985	814	-989	-4727	-64	-1586	1888	-593	575	-1209	-108	-2137	44	-976	-1423	-464	933	-1843	-2567
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-2	-13024	-9622	-732	-1329	-1606	-575	*	*											
24	-583	-1822	-527	280	-3015	-1004	-2221	453	-593	1039	-18	700	-3287	-217	309	-150	-503	1325	-1842	-2914
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

-	-5	-13022	-8266	-732	-1329	-1746	-511	*	*											
25	219	-2780	-552	436	-1437	55	-1029	417	-290	122	-922	696	-1366	-127	52	332	-790	933	-2081	-916
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-13017	-7273	-732	-1329	-1121	-888	*	*											
26	-1020	-1945	-605	-79	-1855	30	-1414	967	-799	345	352	995	-1776	-612	-1351	-1416	274	1796	-4937	-2905
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-13014	-8255	-732	-1329	-1422	-674	*	*											
27	-632	-1945	279	266	-3131	543	621	-1355	334	-931	-2279	2319	-1781	-388	24	-597	-145	319	-1879	-1952
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-35	-13014	-5396	-732	-1329	-1012	-988	*	*											
28	-980	-1922	-179	-93	-2701	1615	326	-406	-1207	-603	260	849	-687	126	-253	52	-140	843	-4912	-2878
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-29	-12989	-5664	-732	-1329	-1928	-440	*	*											
29	-454	-1122	72	29	-3078	-356	186	-358	13	-348	402	1020	-1870	442	-207	-123	920	1028	-4891	-1621
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-12967	-7751	-732	-1329	-2558	-269	*	*											
30	-278	56	454	-148	-1464	544	-147	-762	-417	-546	-435	224	645	60	472	628	-349	315	-1777	-1562
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-20	-12965	-6217	-732	-1329	-2610	-258	*	*											
31	-141	-1772	-30	-225	-431	-209	321	17	-621	650	153	-960	-1190	-243	-730	-672	277	1533	-1760	-1001
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-14	-12950	-6744	-732	-1329	-3036	-188	*	*											
32	-8	-1091	333	840	-2309	-243	213	-398	-292	-439	-168	-304	-608	452	516	211	471	282	-4864	-534
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-21	-12938	-6115	-732	-1329	-2742	-234	*	*											
33	361	-3616	-66	214	-1650	563	785	-891	-135	-159	-2192	1058	-2865	-35	-371	84	536	637	-1788	-2469
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-15	-12925	-6587	-732	-1329	-3459	-138	*	*											
34	376	-1022	-746	-521	-1238	-1340	1492	-79	331	49	908	-2429	-2211	169	-57	-73	729	974	124	-605
-	206	973	-176	-351	-41	369	588	-636	437	-130	-677	-165	39	-73	-330	-53	32	-10	-261	-99
-	-6708	-57	-5109	-4	-8558	-3141	-174	*	*											
35	569	-1778	501	184	-938	-1087	2300	-224	-347	489	-285	-255	-3379	242	-767	-732	-466	693	-4781	-1155
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-13	-12853	-6848	-732	-1329	-2776	-228	*	*											
36	519	-503	171	1090	-701	-2467	240	-508	178	208	-637	-1423	-2198	419	-658	-295	413	910	-1668	-1108
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-43	-12855	-5093	-732	-1329	-3498	-134	*	*											
37	481	-486	270	907	-464	-2088	1163	-330	72	155	-796	-387	-3066	1085	733	-1281	-681	591	-4748	-3621
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-50	-12818	-4875	-732	-1329	-4511	-65	*	*											
38	1196	-866	-821	84	-4479	-2023	-43	376	596	18	-955	-935	-1854	259	504	-702	-632	1243	-1322	-1745
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-	-60	-12766	-4633	-732	-1329	-4193	-81	*	*											
39	507	-707	-328	230	-2053	-1116	-2936	-34	606	247	-469	-419	-2947	750	263	-519	-631	1376	-1991	-886

-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-65	-12710	-4511	-732	-1329	-4982	-46	*	*											
40	1013	-3344	164	-211	-2722	-913	-237	803	235	212	72	-25	-2391	267	550	-292	-307	201	-4579	-1904
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-37	-12641	-5329	-732	-1329	-4573	-62	*	*											
41	618	-1495	-2706	-51	-515	322	-3706	1012	318	329	98	-501	-1677	-681	442	-1069	202	698	-4545	-1496
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-49	-12606	-4913	-732	-1329	-4485	-66	*	*											
42	101	210	-2192	-582	-1748	-246	-1163	928	683	1242	-165	-615	-823	-301	3	-152	117	-736	-4504	-1618
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-	-41	-12563	-5168	-732	-1329	-4585	-61	*	*											
43	492	180	-617	-114	-2600	-1321	-525	-24	1469	-284	-601	-530	-1811	750	791	-55	-156	308	-4472	-1192
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-44	-12529	-5053	-732	-1329	-4612	-60	*	*											
44	295	-924	-924	524	-4214	-171	-1248	-1134	-1	653	-705	807	80	150	-1304	103	225	693	-4433	-1358
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-	-6451	-19	-9305	-5	-8177	-5528	-32	*	*											
45	-645	-1338	-1218	229	-2598	1280	-786	-793	391	-133	335	-13	-455	-128	-171	240	428	373	-4410	-359
-	204	976	-178	-351	-40	371	584	-632	435	-132	-679	-167	39	-69	-331	-52	33	-7	-260	-100
-	-6430	-59	-5124	-6	-8037	-5596	-30	*	*											
46	-889	-3035	-2081	-38	-1544	-593	344	-44	741	696	-1756	-1468	47	-533	24	-312	775	1369	-4269	-1859
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-64	-12312	-4536	-732	-1329	-5219	-39	*	*											
47	-1226	-1116	-3071	-842	-1381	-1469	-962	684	8	801	480	-774	-923	14	-436	-702	360	2001	-4203	-2051
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-111	-12241	-3758	-732	-1329	-5925	-24	*	*											
48	-530	-948	-1461	-823	-2766	-3450	42	398	301	758	221	-842	-1907	-32	1245	-328	1089	766	-4077	-488
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-143	-12104	-3412	-732	-1329	-6060	-22	*	*											
49	-1974	-798	-2251	-671	-1466	-2087	-2373	813	-276	1965	233	-1810	-3615	-1383	-129	-651	-773	1272	-3910	-348
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-156	-11919	-3289	-732	-1329	-6200	-20	*	*											
50	-1488	-652	-2783	-293	-1864	-1028	-137	668	948	126	-1067	-479	-3436	89	1252	-1077	494	1492	-3732	-954
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-274	-11717	-2532	-732	-1329	-6349	-18	*	*											
51	-76	-1582	-1390	-1057	-950	-2796	-2583	1625	158	1054	-1657	-3332	-3128	-1433	1259	-1024	-1718	1396	-3423	-787
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-367	-11360	-2158	-732	-1329	-6574	-15	*	*											
52	-253	593	-1371	688	-1959	-1492	-2207	-187	675	-112	-1805	-2476	-2752	1237	1856	-1388	-1700	1062	61	-764
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-365	-10905	-2165	-732	-1329	-6817	-13	*	*											
53	-514	-1451	-1655	-269	-1694	-2058	-1845	114	879	27	-3106	-2594	-2389	-2503	2887	-848	-1819	-135	-2685	447
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-	-925	-10429	-1082	-732	-1329	-6977	-11	*	*											

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54   -525   1237   -1982   432   -1839   -296   -1218   -1558   1150   -1933   -2480   -196   -1763   1027   2491   -1857   20   -1815   -2058   761
-    *      *      *       *     *       *      *       *       *      *       *       *      *       *      *      *       *    *       *       *
-    *      *      *       *     *       *      *       *       *      0
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NAME doma.txt
DESC
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ALPH  Amino
RF    no
CS    no
COM   [converted from an old Plan9 HMM]
NSEQ  0
DATE  Mon Mar  8 11:44:03 1999
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NULE     595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM        A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y
         m->m   m->i   m->d   i->m   i->i   d->m   d->d   b->m   m->e
        -3130      *   -175                 ,
     1   -235    539   -619   -793    463    -69    144    371     -3    301    634   -605   -400    545   -776   -495   1111   -453   -695    537
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12    255     97
     -    -13  -7388  -8388   -732  -1329  -3508   -133  -3130      *
     2    308    539   -619      4    539    -69    144   -205     -3    627  -1117    178    445   -513   -776   -495   -414     93   -695   -537
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -13  -7388  -8388   -732  -1329  -3010   -191      *      *
     3   -289    485   -673     17   -530   -122     91   -710    523    -54    420    717   -454   -567   -829    740    456      7   -749   -591
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -12  -7519  -8519   -732  -1329  -3171   -170      *      *
     4     99   1519   -701   -875   -559    328     62    -71    -85   -653  -1199    776    888   -595   -858    360    257   -535   1462    619
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -11   7588  -8588   -732  -1329  -3409   -143      *      *
     5     21   1603   -701   -875    472   -151     62    -73    -85    253    596   -687   -482   -595   -858    419     95    629   -777    619
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12    255    -97
     -    -11  -7588  -8588   -732  -1329  -3409   -143      *      *
     6    310    457     -5      3    470   -151     62   -307    -85   -653    709   -687   -482   -595   1452   -177    -19   -535   -777    619
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -11  -7588  -8588   -732  -1329  -3409   -143      *      *
     7   -310    457   -126    525   -559    -31     62  -1158    -85   -653    696   1100   -482    746    137    190    212   -535   -777   -619
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -11  -7588  -8588   -732  -1329  -3409   -143      *      *
     8    865   1620   -701   -875   -559   -151     62  -1158    277   -653  -1199    316    715    233   -858     97    257    219   -777   -619
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
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     9    -10   1618   -701   -875   -559   -151     62   -103    -85   -223   1330   -687   1075   -595   -858    -73    713     23   -777   -619
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -11  -7588  -8588   -732  -1329  -3409   -143      *      *
    10    230    457   -701   -209   -559    346    794  -1158    -85   -653   1900    488   -482   -344    153    688   -496   -535   -777   -619
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     -    -11  -7588  -8588   -732  -1329  -3409   -143      *      *
    11   -317    457   -126   -106   -559    394     62  -1158    499   -653    391   1429   -482   -595    151    420    -18   -535   -777   -619
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     -    -11   7588  -8588   -732  -1329  -3409   -143      *      *
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41		-335	-54	27	-12	-255	97
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13	-317	457	-701	-875	-559	-151	62	796	344	666	-397	-676	897	83	858	-71	-496	23	-777	-619
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	73	-335	-54	27	-12	-255	97
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16	106	457	-701	-875	233	-151	794	902	-85	-489	-302	330	353	-344	-858	-91	-496	591	777	202
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18	-317	457	6	-875	207	346	62	138	930	-653	126	506	-482	-595	32	622	-318	535	777	-619
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-	11	7588	8588	732	1329	3409	-143	*	*											
22	21	457	-31	542	-559	404	62	-1158	514	-225	-1199	94	149	432	32	-577	202	-97	-777	-619
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25	104	1603	-701	655	-559	402	62	-307	53	-653	-1199	-687	-482	1022	-858	526	178	-535	-777	-619
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26	83	457	-126	1	-559	-151	1121	-1158	-85	-653	-1199	-687	543	976	-858	1004	277	-535	-777	-619
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27	169	1586	-701	-875	472	244	1205	-320	499	-653	-1199	-687	-279	-595	-858	404	275	-535	-777	1063
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28	-344	1592	299	256	892	-178	35	174	-112	176	-1227	-714	-243	-623	-885	-119	174	-562	-805	590
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29	141	1590	-729	-259	-586	-178	35	-1185	875	-337	-1227	171	-510	1473	94	-604	481	-562	805	647
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30	-404	369	585	-962	-646	-238	1134	-1245	190	675	-1287	19	-569	1384	-171	-57	-583	-106	865	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
31	-404	1285	524	46	116	-238	1132	-308	1	13	-1287	-774	-569	-683	326	-1	114	-87	-865	548
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
32	124	369	41	-318	-646	-238	-25	-1245	272	557	-404	-535	-569	-613	-362	-429	1259	-184	865	546
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-	-70	-7794	-4535	-732	-1329	-3313	-153	*	*											
33	-378	396	552	-386	-619	-211	1	-370	769	-714	-1260	1065	-543	403	-918	19	214	322	838	143
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-	-10	-7735	-8735	-732	-1329	-3346	-149	*	*											
34	165	2276	-762	-167	198	-211	1	-381	443	-380	-1260	46	-543	401	-918	960	-557	596	838	-680
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7735	-8735	-732	-1329	-3346	-149	*	*											
35	397	1532	-762	-738	-619	504	1060	-1219	-146	-370	489	-310	122	-656	-292	566	216	95	-838	-680
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7735	-8735	-732	-1329	-3346	-149	*	*											
36	-378	396	693	-936	-619	121	1144	-228	307	-714	-1260	885	-543	-656	-918	-146	971	-596	-838	969
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-10	-7735	-8735	732	1329	-3346	-149	*	*											
37	397	1758	649	960	-619	-211	752	311	39	-714	270	-748	-543	-656	68	-638	-557	-596	-838	680
-	206	979	178	352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	10	7735	-8735	732	1329	-3346	-149	*	*											
38	397	396	683	936	784	-211	1	141	453	-714	-741	-748	-543	-656	61	818	-78	-576	-838	-680
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-	-10	7735	-8735	-732	-1329	-3346	-149	*	*											
39	126	396	-89	234	758	-211	1161	-368	299	-158	-1260	-748	-543	-656	-134	164	-557	261	-838	434
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-	-10	-7735	-8735	-732	-1329	-3346	-149	*	*											
40	744	396	-202	-270	-619	-211	1159	-132	216	-284	-1260	60	-543	-656	-918	668	196	48	-838	-680
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-10	-7735	-8735	-732	-1329	-3346	-149	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7735	-8735	-732	-1329	-3346	-149	*	*											
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-	-10	-7735	-8735	-732	-1329	-3346	-149	*	*											
43	713	396	-749	1	1185	-111	1	-1219	-146	-201	-1260	-748	-543	-3	252	-638	-379	1006	-838	-680
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7735	-8735	-732	-1329	-3076	-182	*	*											
44	956	369	-788	207	-646	-238	-25	-1245	1219	-179	-1287	-421	-569	251	-945	-640	528	92	-865	707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-10	-7794	-8794	732	1329	-3313	-153	*	*											
45	627	369	-81	223	646	-238	-25	844	417	69	1287	244	185	-683	945	-664	-583	91	-865	707
	206	979	178	352	36	372	585	635	438	-130	-677	-164	41	-73	335	-54	27	12	-255	97

-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*										
46	550	369	13	-962	353	-238	-25	-262	-172	389	-1202	242	-569	-340	638	254	-405	87	885	-707
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47	148	369	-100	442	-646	495	-25	-1245	771	117	-1287	-730	266	-683	63	-179	-583	359	865	707
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-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*										
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49	-404	369	-788	-690	-646	171	-25	1063	833	386	-1287	-774	-569	-5	-945	263	-583	-387	865	911
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50	197	1310	-76	-136	198	134	15	-1206	374	-139	-1247	347	-530	-643	-894	28	-544	113	-825	1433
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51	-404	1823	-652	1115	-646	-124	272	-1245	280	-170	-1287	-447	-569	-683	385	-12	-583	-87	-865	1131
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-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*										
52	963	369	-788	633	-391	-238	-25	385	366	-570	850	-774	-569	-683	-945	-664	-583	390	-865	530
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*										
53	-404	369	-788	486	-601	187	-25	1072	733	404	-1287	-774	-569	-683	-945	-12	-22	-622	-865	60
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	10	7794	8794	732	1329	3313	-153	*	*										
54	404	369	788	547	816	171	416	629	-172	509	-1287	-18	-569	314	-945	-664	-583	-622	-865	563
	206	979	178	352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	10	7794	8794	732	1329	3313	153	*	*										
55	689	369	788	167	646	534	-25	-232	586	-179	-1287	-774	272	-683	-945	-161	-414	-460	-865	1207
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*										
56	-404	369	-788	-99	1015	-238	-25	176	741	-189	-1287	122	-569	132	-945	-253	623	-622	-865	938
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*										
57	19	1986	-788	-318	-646	-238	-25	392	1278	-333	-1287	213	-569	-5	-171	-264	176	-622	-865	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*										
58	-4	1498	-788	-641	-646	-238	1001	442	-165	-169	508	-774	-569	346	964	-7	-583	-78	-865	272
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*										
59	711	369	-788	-84	262	179	884	-1245	822	-170	621	-774	-569	-683	-945	-7	-22	22	-865	115
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*										
60	142	369	-788	663	451	-238	-25	-1245	-172	-3	-1287	213	-569	1051	-56	-664	189	80	-865	413
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*										
61	379	369	-788	-167	262	495	-25	-870	-172	255	-1287	-774	62	719	-945	319	289	-65	-865	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	1329	-3313	-153	*	*										
62	717	1285	-788	63	-646	94	-25	-160	-159	-184	644	-675	-44	807	-945	-55	114	-87	-865	-707

-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
63	-170	369	-228	655	-646	301	-25	-1245	-172	-740	641	565	-569	-683	434	-383	533	673	-865	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
64	138	369	-788	422	-646	-238	-25	-1245	-172	355	463	-774	-569	377	839	254	-414	374	-865	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
65	-4	369	-547	-84	-646	417	-25	-394	-172	333	-1287	1241	-569	375	623	-664	-583	-622	-865	272
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
66	-404	1506	-788	310	-646	179	1034	-1245	768	-179	-1287	-774	-569	-3	-945	-264	189	346	-865	1258
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
67	333	369	-788	-962	-646	316	1117	-1245	-172	-740	-1287	849	-569	-683	501	285	543	68	865	845
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	-97
-	-70	-7794	-4535	-732	-1329	-3313	-153	*	*											
68	-378	1630	-762	-86	-619	333	285	-407	373	-714	535	1069	-543	172	924	-638	-557	61	-838	680
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	73	-335	-54	27	-12	-255	-97
-	-10	-7735	-8735	-732	-1329	-3346	-149	*	*											
69	802	396	67	-664	-619	-211	1	-925	-146	431	1256	9	-543	-656	534	-638	-557	367	-838	680
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7735	-8735	-732	-1329	-3346	-149	*	*											
70	169	396	312	428	-619	-211	1161	-1219	180	207	1069	-748	-543	-656	-918	14	484	-596	-838	313
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	-97
-	122	7735	-3714	732	1329	-3346	-149	*	*											
71	331	443	-375	559	-329	390	1206	-433	799	-667	703	-701	655	-610	-872	366	-510	-549	791	-633
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	11	7627	8627	-732	-1329	3132	-175	*	*											
72	289	415	-742	-916	-600	597	21	-1199	-126	650	1291	28	-523	-637	-899	654	-537	68	-819	-661
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-11	-7691	-8691	-732	-1329	-3370	-147	*	*											
73	-341	415	172	-916	-600	225	21	-387	-126	623	1182	-706	-523	-637	88	-568	-537	640	-819	890
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-11	-7691	-8691	-732	-1329	-3370	-147	*	*											
74	-358	415	170	-916	-600	-192	21	-240	787	424	691	-489	109	44	-899	300	-537	-32	-819	559
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-11	-7691	-8691	-732	-1329	-3101	-179	*	*											
75	-385	388	-769	343	-627	-219	74	-1226	553	-160	950	585	-550	-664	1117	365	-564	-89	-846	-687
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7752	-8752	-732	-1329	-3339	-150	*	*											
76	-385	388	-769	1216	378	-219	-6	-1226	-153	-202	-1267	-755	-550	854	-926	300	-564	570	-846	550
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7752	-8752	-732	-1329	-3339	-150	*	*											
77	162	388	60	518	-627	-219	865	-1226	303	244	-1267	-755	-550	821	430	-645	-564	110	-846	306
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7752	-8752	-732	-1329	-3339	-150	*	*											
78	385	388	131	569	754	-219	-6	-235	-153	619	-1267	-755	-550	271	-926	12	-564	-390	-846	860
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
-	10	-7752	-8752	-732	-1329	3339	-150	*	*											

79	527	388	-769	260	311	115	1501	-155	797	-151	-1267	1	-550	-664	359	-645	-564	603	-846	-687
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
-	-10	-7752	-8752	-732	-1329	-3133	-175	*	*											
80	-404	369	-788	320	369	-238	1034	-191	256	116	-1287	-774	-569	377	1028	-664	-583	544	865	707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
81	-404	2462	126	-962	-646	-238	1117	-985	366	6	889	-774	-569	375	95	198	-583	-622	865	520
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
82	-404	369	124	-285	119	241	-25	297	417	487	-1287	-774	-569	-683	34	226	-583	-106	-865	520
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
83	250	369	13	-962	1137	-238	-25	680	-172	-228	-1287	-774	-569	132	41	343	-583	-184	865	564
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
84	370	369	-788	-112	808	-238	1519	-1245	-172	109	1685	7	-569	-683	-945	-664	-583	74	865	756
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
85	100	1880	13	-962	145	-238	1132	-434	416	451	621	-126	-569	-683	262	-664	-583	-622	865	242
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
86	148	1431	-788	-106	541	-238	-25	-985	740	54	-1287	-774	-569	345	-945	874	583	143	-865	707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
-	-10	-7794	-8794	-732	1329	-3313	-153	*	*											
87	714	2092	-788	-962	-646	-238	-25	-1245	272	369	867	213	-569	-683	-945	848	-583	-622	-865	707
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88	-404	1515	754	726	-646	241	-25	-184	190	431	644	-774	-569	-683	-945	-12	-583	-622	-865	707
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-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
89	346	1506	-788	261	-646	-238	-25	-1245	257	750	641	213	-569	105	-945	-186	-414	-1	-865	707
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-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
91	142	2166	-93	-194	-646	-238	-25	545	-172	474	-707	577	-569	-683	-158	-664	-583	22	-865	707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
92	370	1530	-213	214	-646	-238	1001	-1245	191	436	-1287	659	-569	105	-945	-664	-583	495	-865	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
93	309	369	13	-84	292	-238	-25	-407	-172	794	-1287	-126	-569	142	-945	56	547	-622	-865	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
94	458	369	-788	1045	814	-238	1481	583	-172	-740	-1287	-774	-569	352	-945	-664	164	-622	-865	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
95	148	369	-788	-411	649	-238	873	278	908	-740	-1287	220	266	554	-945	-664	-414	92	-865	442
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*										
96	-404	369	-788	-632	-646	-238	1416	-1245	635	224	283	19	-569	-683	-51	406	457	91	865	530
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	255	97
-	-90	-7794	-4153	-732	-1329	-3313	-153	*	*										
97	-369	404	-754	-927	868	-203	10	-1210	291	258	-1252	683	-535	-648	739	371	-71	381	830	672
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
-	-106	-7714	-3921	-732	-1329	-3354	-148	*	*										
98	232	444	-714	-887	458	-163	50	250	331	302	-1212	-700	-495	-608	-870	911	-509	488	-790	-632
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	255	-97
-	-171	-7619	-3232	-732	-1329	-3397	-144	*	*										
99	294	507	-651	-824	-508	222	395	-1108	418	410	-1149	937	200	-545	-58	-115	-446	-485	727	686
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
-	-12	-7459	-8459	-732	-1329	-3458	-138	*	*										
100	149	507	397	417	-508	14	113	-938	-34	415	-1149	358	-432	-545	-807	148	-446	124	-727	684
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
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101	512	1452	-607	-137	-465	-57	467	-253	9	303	479	-593	-388	-27	216	191	-402	-441	684	-525
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
-	-141	-7346	-3524	-732	-1329	-3502	-133	*	*										
102	238	2044	932	-736	581	-12	201	-1019	54	-514	-1060	655	-343	-457	-719	-438	396	-396	-638	-480
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
-	-15	-7219	8219	-732	-1329	-3540	-130	*	*										
103	160	1626	146	736	238	-12	1328	-1019	54	658	-482	-548	499	-457	-719	-438	-357	-396	-638	-480
-	206	979	-178	352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-15	-7219	8219	732	1329	3540	-130	*	*										
104	178	596	562	69	420	-12	201	-1019	483	793	-1060	246	-343	-457	262	373	-357	-396	-638	480
-	206	979	178	352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-15	-7219	8219	732	1329	3540	-130	*	*										
105	-178	1726	-562	381	-420	311	201	-167	266	42	-1060	411	-343	-457	30	-438	-357	247	-638	480
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	-97
-	-15	-7219	-8219	-732	-1329	-3540	-130	*	*										
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-15	-7219	-8219	-732	-1329	-3203	-166	*	*										
107	-217	556	-602	-776	-459	-51	1075	444	14	403	471	407	-383	-496	-758	130	-397	486	-678	-520
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-121	-7331	-3751	-732	-1329	-2710	-239	*	*										
108	551	485	-673	421	-530	-122	91	-1130	-57	-625	1961	-8	328	-567	-80	115	-468	9	-749	-591
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-12	-7520	-8520	-732	-1329	-3442	-139	*	*										
109	49	1614	-525	-847	-530	-122	782	-1130	-57	-625	1207	-128	395	403	1000	-36	114	-507	-749	-591
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-	-12	-7520	-8520	-732	-1329	-3117	-177	*	*										
110	162	450	135	-238	1269	-158	55	-1165	337	-230	-1206	-523	-489	-603	130	198	507	-542	-785	353
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111	507	409	-749	-279	875	-198	1148	-6	-133	-270	-1247	-735	622	-643	-905	385	216	-583	-825	155
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	97
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112	632	369	97	-962	1599	94	-25	-1245	-172	-740	-1287	-774	774	-683	483	403	-583	622	-865	-707

-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
113	-404	1994	-788	-962	-646	-238	1823	-1245	-172	101	-1287	-19	819	-683	420	-161	-583	346	1296	-707
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
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-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
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-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
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-	-10	-7794	-8794	-732	-1329	-3313	-153	*	*											
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123	-332	441	950	-890	364	-166	47	-900	-100	714	-1214	109	352	-611	-873	-79	-34	209	-793	-634
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
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127	375	434	-723	-897	1226	-173	40	241	857	-675	-1221	-709	753	-618	-880	42	-182	-557	-800	595
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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128	-671	103	-1055	-1229	445	-504	-291	-91	151	-1007	-1553	-1041	263	-121	-1211	1749	-96	-244	784	1167
	206	979	-178	-352	36	372	585	635	438	-130	-677	-164	41	-73	-335	-54	27	12	255	-97
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129	-540	111	-1047	-52	643	-489	-283	-30	23	-999	-1545	-238	-828	-941	-1203	-362	2050	289	551	288
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131	-115	173	-276	-294	511	-435	-222	-1442	461	-592	-1483	-35	-766	2557	-1142	-758	-767	-174	-1061	350
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
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134	-643	131	2147	-321	905	-18	1242	205	-411	-979	-1525	-231	-808	-494	-264	-903	-230	-861	-1103	-945
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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136	-82	451	1009	395	-867	1932	-246	-1107	53	-213	-1507	-995	-790	-903	-1166	-221	-791	655	-1085	-927
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137	231	126	881	149	-889	-481	-268	-398	-52	-983	-1530	-1017	-56	-926	-1188	162	2257	308	-1108	-950
	206	979	178	352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	7	8304	9304	732	1329	3022	190	*	*											
138	301	126	2141	341	421	17	759	-402	-415	148	-1530	-259	-812	-926	-3	-660	-826	-865	-1108	-950
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	7	8304	-9304	-732	-1329	3022	-190	*	*											
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140	-706	67	-514	-384	-156	-540	700	-1547	-474	-480	310	-1076	-871	-985	82	2070	26	-924	771	-58
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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142	-706	67	-260	-388	61	400	-327	-1547	-29	378	-1588	-1076	2202	-985	268	-966	-885	-924	-1167	545
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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143	-706	67	-190	-1264	-948	13	-327	-1547	1029	-76	207	-282	358	-985	-1247	-543	-712	-388	4036	-1008
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144	-176	51	-1107	-1281	939	-556	-343	2019	-491	-488	303	-1093	-888	-1001	65	-307	-154	603	-1183	-1025
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-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
145	-180	51	-1107	-615	-964	-556	1162	-203	48	1466	-1605	-1093	768	-1001	-252	-309	-902	228	-1183	-1025
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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	6	8440	-9440	-732	-1329	-2839	-217	*	*											
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	-6	8440	-9440	-732	-1329	-2839	-217	*	*											
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-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
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159	-218	51	-1107	-431	-160	-556	528	2263	-491	-86	-250	-1093	-888	-213	-1263	-983	-902	-319	1602	451
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
161	-723	51	-1107	123	-964	-556	555	-753	1023	-1059	-1605	-1093	-888	-1001	-1263	1825	301	232	1101	-1025
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-6	8440	-9440	732	1329	-2839	-217	*	*											
162	-300	51	1107	-1281	2422	207	1100	420	-491	138	-1605	441	-888	-1001	-1263	-309	-142	-941	-1183	-1025

-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
163	-160	51	-434	655	43	-556	-343	1921	-491	54	-1605	446	-53	-1001	-1263	-65	902	941	1183	-1025
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
165	1797	952	-1107	-431	144	-556	-343	-1564	-491	-273	-74	-299	-888	-67	84	33	-653	314	1123	1025
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-	-6	-8440	-9440	-732	-1329	-2839	-217	*	*											
166	-171	805	-1107	1918	-964	-556	1290	488	-491	105	-1605	-745	-888	-1001	-1263	-983	-131	-425	1183	591
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168	-234	99	-772	468	-917	-509	1445	-1516	-443	-1011	-1557	2246	-840	-954	554	439	854	-796	1149	977
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-	-100	-8354	-3965	-732	-1329	-2937	-202	*	*											
170	365	148	444	-983	-867	-55	246	-106	36	550	809	-996	-342	-904	-1166	-885	1865	-844	-1086	-928
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-533	-8261	-1710	-732	-1329	-178	-3106	*	*											
171	-1053	599	-1437	2679	-1295	-453	388	-1038	-821	-142	-574	-340	-371	-538	-744	-965	-1232	-1271	806	-1355
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-4	-9006	-10006	-732	-1329	-1444	-661	*	*											
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174	68	-317	-1475	-795	-1332	-924	-711	-90	-858	157	-1973	-1460	-1255	-1369	3030	-586	-1269	-1308	-1551	-1393
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-	-37	-9064	-5398	-732	-1329	-1801	-488	*	*											
177	-506	625	-1453	-1626	-1310	-902	451	-636	-315	-35	-1951	3086	-1234	-664	-612	-312	-1248	-350	-1529	-1371
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-	-42	-9030	-5215	-732	-1329	-1907	-448	*	*											
178	-478	-271	-729	217	-1286	-878	-665	-1885	214	-422	-1926	-1414	-1209	-529	-1585	2576	-547	-1262	-1505	-1347
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	255	-97
-	-32	-8992	-5649	732	1329	-2015	410	*	*											

179	-464	-253	-831	-731	-1268	-860	1667	-1867	-273	2152	-1909	207	-1192	-13[illegible]	-174	-780	1206	-1244	-1487	-991
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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181	-1000	-227	-1385	2820	-1242	-834	-621	-986	-768	-474	8	-68	-63	-1279	-530	-771	1180	-1218	-1461	-1303
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-	-46	-8924	-5082	-732	-1329	-2186	-358	*	*											
182	-430	-201	-1358	-669	-420	-808	979	-1815	-742	-560	-259	-1344	-1139	3384	-496	-499	-1153	-1192	-1435	-1277
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-	-8	-8882	-8061	-732	-1329	-2277	-333	*	*											
183	-972	593	-656	-253	-551	-805	-592	2968	-740	-1308	-1854	-1342	-1137	-1250	-171	-1231	-1151	-1190	1594	-1274
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-	-5	-8878	-9878	-732	-1329	-2285	-331	*	*											
184	-972	-198	-191	494	-1213	-805	-592	-379	-740	2248	-1854	-1342	-1137	-208	-1512	-716	-1151	-1190	-1432	-1274
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185	-972	-198	-1356	2844	-1213	-805	196	-718	-158	-346	540	-1342	-1137	-1250	-620	-1231	-1151	-1190	-1432	-1274
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191	-972	-198	-1356	-976	-443	-805	-592	-1813	2851	135	-1854	171	-1137	-1250	-734	-716	-1151	-1190	850	-1274
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192	21	-179	-1337	-648	-1195	2677	-574	-1794	-721	-1289	-1835	-1323	-449	-1232	-217	313	-1132	-1171	-1414	-1255
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193	-872	-99	-1257	-1430	-1114	-706	-493	-1713	-51	-346	-1755	-1242	-1038	-1151	-1413	2652	-1051	-1090	2215	-1175
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194	-442	-71	-1229	-1403	-278	-134	-465	-1686	105	-1091	-1727	-1215	-1010	-833	-1055	2681	-869	-1063	-1305	-1147
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-	-5	-8668	-9668	-732	-1329	-2634	-253	*	*											
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200	-31	743	-415	-589	127	136	349	-872	201	-367	-913	-401	-196	-309	-571	713	-210	-249	2699	93
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203	19	793	365	-539	-222	186	398	755	251	-199	-863	-351	-146	-259	267	-241	160	319	441	283
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204	495	868	290	464	148	260	725	747	538	-242	-788	-276	-71	-151	398	-166	-85	124	366	208
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-	-29	6236	7236	732	1329	3735	113	*	*										
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206	495	868	-290	-464	-148	260	473	-747	326	-242	-788	357	196	-184	-447	70	93	-124	-366	208
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
-	-29	-6236	-7236	-732	-1329	-3735	-113	*	*										
207	210	868	-290	72	-148	260	473	-747	414	-242	-788	-276	-71	606	80	-166	-85	-124	366	208
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-	-220	-6236	-2961	-732	-1329	-3735	-113	*	*										
208	132	905	-116	30	-110	298	511	-709	364	-204	-750	554	-33	-147	-409	-128	-47	-86	-329	171
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-	-59	-6047	-5326	-732	-1329	-3757	-111	*	*										
209	137	910	-247	-421	-105	303	516	-704	385	-199	-745	-233	-28	-142	717	-123	-42	-81	-324	166
-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
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//

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DESC
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ALPH  Amino
RF    no
CS    no
COM   [converted from an old Plan9 HMM]
NSEQ  0
DATE  Mon Mar  8 11:44:31 1999
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NULT       -4  -8455
NULE      595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM         A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y
          m->m   m->i   m->d   i->m   i->i   d->m   d->d   b->m   m->e
         -2829      *   -219
      1     81    256   -902  -1075   -759   -351   -138    -75    687   1392  -1400   -887   -683    323   -407    403   -696   -735   -978   -820
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -8  -8054  -9054   -732  -1329  -3255   -160  -2829      *
      2    444   1482   -498  -1075    462   -351   -138  -1358   -285   1374  -1400    279    250   -796  -1058   -777   -696   -735   -978    500
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -   -102  -8054  -3948   -732  -1329  -2863   -213      *      *
      3   -507    267    225  -1065    472    340   -128  -1348    -17   -156  -1389   -877   -672    147   -325   1476    686    220   -968    169
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27     12   -255     97
      -     -8  -8030  -9030   -732  -1329  -2809   -222      *      *
      4    406    223    935   1780   -792   -384   -171  -1392    213    -53  -1433   -921   -716   -829    235    173    259    648   1011    853
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335     54     27     12    255     97
      -     -8  -8119   9119   -732  -1329  -2769   -229      *      *
      5   -446    182    975   1149    129   -425   2716  -1432    370    153  -1473   -505   -756    249    460    407    486    809   1052    894
      -    206    979    178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27     12    255     97
      -    -32  -8200   5758   -732  -1329  -2867   -213      *      *
      6   -600    174    984  -1158   -842    -76   -221    461   -368     39  -1482    821   1664   -878    335   -537    565   -818  -1060    273
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     99  -8217  -3995    732  -1329  -2957   -199      *      *
      7   -566    207    951   1619   -808   -400   1532   -643    220   -207  -1449   -936   -492   -845    715    -17    359   -784  -1027   -869
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -8  -8150  -9150   -732  -1329  -2686   -244      *      *
      8   -612    162    100    -97   -854   -446   -233   -250   1080   1455  -1494   -982   -777   -147    -85   -872   -210   -830  -1073   -914
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -7  -8240  -9240   -732  -1329  -3095   -180      *      *
      9   -315   1386   -996   1286    289   -446   -233    162   -380    742  -1494   -982   -777   -581   -213   -318   -791    355  -1073   -914
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -7  -8240  -9240   -732  -1329  -3095   -180      *      *
     10     73   1537   -996   -241    989   -446   2695   -558   -380   -257  -1494   -982   -777   -891    283   -872   -791   -830   1462    995
      -    206    979   -178    352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -7  -8240  -9240   -732  -1329  -3095   -180      *      *
     11     73    162   -996   1170   1314   -446   -233   1629   -133   -948  -1494     94   -777   -891    969   -115    104   -830  -1073   -914
      -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
      -     -7  -8240   9240   -732  -1329  -3095   -180      *      *
     12   -612   1485   -996  -1170   -331   -446   -233   1695   1176    277  -1494   -982   -777   -891   -379   -417   -791    -71  -1073    205
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	206	979	-178	352	-36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	12	-255	97
	7	8240	-9240	-732	1329	3095	180	*	*											
13	94	162	996	1170	908	446	-233	467	501	368	1494	982	777	-891	581	872	791	830	3489	-914
	206	979	178	352	-36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	12	255	97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
14	-612	162	100	-159	854	-446	-233	195	836	-20	-1494	-982	-777	-891	-519	155	1546	-830	1563	261
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	3095	-180	*	*											
15	-612	696	-996	-241	326	-446	-233	-162	295	1172	-1494	-982	-777	228	45	-369	422	135	-1073	-914
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
16	-612	1559	-996	-505	1971	-446	988	-306	21	-304	-1494	225	-777	-891	-211	-50	104	-830	-1073	956
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
17	22	162	100	-788	703	-446	1210	-1453	-380	924	-1494	-982	136	1877	-755	-872	-791	-830	-1073	-720
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-95	-8240	-4052	-732	-1329	-3095	-180	*	*											
18	318	1574	-952	843	-347	-401	2740	-1409	-336	-121	-1450	12	-80	-846	-1108	-827	-277	44	-1028	-870
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-8	-8152	-9152	-732	-1329	-2694	-242	*	*											
19	497	162	-301	484	394	-304	1087	-250	-380	-340	-1494	-982	-777	228	-1153	-872	1719	-830	-1073	-914
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
20	-118	1485	-996	-241	-854	-377	-233	-688	-380	1427	-1494	-982	-777	228	641	-578	160	-830	-167	-194
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
21	612	1249	-996	-505	-854	-446	988	-250	-270	-22	-1494	-982	217	1877	649	-872	29	526	-1073	-914
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-94	-8240	-4063	-732	-1329	-3095	-180	*	*											
22	-568	206	100	-310	-810	-402	344	133	398	-904	-1450	1762	-80	-847	971	-828	73	98	-1028	-870
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-8	-8153	-9153	-732	-1329	-3161	-171	*	*											
23	-568	740	-952	1330	-810	-402	1205	-109	398	826	-1346	192	-733	-847	243	-828	-747	-786	-1028	-870
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-8	-8153	-9153	-732	-1329	-2697	-242	*	*											
24	-612	1559	-996	-1170	235	-446	-46	240	-380	55	646	-99	-403	793	-298	-745	-791	-830	1324	2161
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
25	-612	2167	330	1286	235	-446	-233	-1453	418	-146	-1494	-982	279	-891	-1153	-745	199	-830	2074	-914
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
26	-612	986	700	-192	-854	-446	-233	-1453	-380	1455	-1494	94	-777	-891	-1153	-248	476	32	-1073	-914
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
27	-612	2265	996	574	311	-446	-233	-1453	-380	38	2600	-982	-777	-891	1017	-872	-321	-830	-1073	-914
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
28	-371	162	430	-1047	819	-446	2074	-1335	-133	-704	740	-982	-777	938	1668	-562	-762	-29	-1073	-914
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-86	-8240	-4201	-732	-1329	-3095	-180	*	*											

29	572	201	1643	48	-814	406	1028	130	733	-240	1454	-942	65	-36	-232	-705	178	-790	-1033	-875
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	164	41	-73	-335	54	27	12	-255	97
-	51	8161	-5004	-732	-1329	-3156	-172	*	*											
30	550	223	1134	392	436	-384	727	-1392	-319	-100	1433	-921	-716	-829	1674	-810	90	-337	-1011	853
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-63	8119	-4672	-732	-1329	-2769	-229	*	*											
31	-565	209	-171	-1123	-806	-398	2824	-1406	-333	235	-1447	-935	-730	1402	755	-3	-162	-783	-1025	-867
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-8	-8149	-9149	-732	-1329	-2650	-250	*	*											
32	-612	1445	-996	-354	-854	-446	1160	92	-380	1440	-1494	-982	-746	617	-1153	-91	-791	213	-1073	-914
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
33	-612	162	1655	-927	-854	-446	852	419	-380	277	-156	93	-777	-76	-1153	-311	-791	-29	-1073	946
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8240	-9240	-732	-1329	-3095	-180	*	*											
34	612	511	347	353	-854	-119	424	-438	-380	132	-35	790	-777	2213	-1153	-872	-791	-830	-1073	-914
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	485	8240	-1826	-732	-1329	-1815	-482	*	*											
35	240	2643	-958	71	-815	-407	-194	1517	-341	-674	-1456	-943	-249	1029	-1114	-833	-752	70	-1034	444
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-8	-8167	9167	-732	-1329	-2817	-221	*	*											
36	58	1399	-848	362	379	-433	-220	-1441	-212	-75	2431	-970	-765	-135	-507	-357	671	-818	1138	-902
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	8215	-9215	-732	-1329	-3111	-177	*	*											
37	-268	174	-984	703	358	-433	-220	-1441	361	854	2431	-970	-716	-878	-1140	-859	385	818	1060	902
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	12	255	97
-	-7	8215	-9215	-732	-1329	-3111	-177	*	*											
38	-599	3109	-984	-223	-841	-433	-220	-1441	-12	672	530	-970	-525	374	435	-859	779	818	1060	1161
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	-12	-255	97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
39	370	1571	984	-913	120	157	98	484	-87	-936	1237	-970	-638	-655	496	1247	-779	-17	-1060	902
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	7	-8215	9215	-732	-1329	-3111	-177	*	*											
40	103	174	17	-1157	-379	-433	-220	-1183	128	-192	2983	-970	-765	485	-367	-681	-779	324	-1060	479
	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	8215	-9215	-732	-1329	-3111	-177	*	*											
41	465	916	479	-109	406	-433	864	-26	-368	-936	-1482	160	-765	-878	-74	-859	-779	-818	-1060	2315
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
42	-599	174	-984	-1157	-841	1307	1001	-948	758	-936	-1482	-258	-765	374	451	-859	-62	-17	2111	597
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	9215	-732	-1329	-3111	-177	*	*											
43	-599	174	-984	-1157	301	-433	1676	1578	-368	39	-469	-970	-765	374	-1140	-455	143	702	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
44	-370	3425	-17	-1157	-120	-433	-220	-1121	308	360	753	-970	-765	110	-1140	-859	687	-818	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
45	103	174	479	-1157	720	-433	-220	-1441	1868	-831	-1482	-20	-765	1322	-1140	-859	150	-818	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

	7	-8215	9215	-732	-1329	3111	-177	*	*										
46	599	174	418	701	-841	433	220	373	380	165	1482	-970	765	1237	1140	859	779	1332	1060	902
	206	979	-178	-352	-36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	-12	255	97
	-7	-8215	9215	-732	-1329	3111	-177	*	*											
47	-599	174	984	388	818	-433	665	-128	1471	194	530	-970	-765	-878	-1140	-859	-449	66	-1060	688
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
48	-599	174	-984	291	379	-433	-220	-1441	-121	506	1103	1646	-765	-878	17	-395	562	-818	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
49	-599	1398	-352	-776	-841	-433	-220	1435	380	145	1237	237	-765	295	-1140	-859	613	-818	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	9215	-732	-1329	-3111	-177	*	*											
50	-599	1965	1456	131	920	-433	-220	-918	-368	-936	347	-970	-765	882	368	-143	-569	-483	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	8215	-9215	-732	-1329	-3111	-177	*	*											
51	90	174	-984	-84	-841	-433	1508	-1441	-368	843	530	-61	-765	973	618	-357	85	-818	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-7	-8215	9215	-732	-1329	-3111	-177	*	*											
52	-599	1163	208	648	-841	-433	-220	516	1471	-936	87	-970	-765	-878	84	-859	553	-818	-1060	417
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-7	-8215	9215	-732	-1329	-3111	-177	*	*											
53	-599	174	106	-1157	1880	156	-220	-294	-368	-292	-1482	-970	-96	-878	515	-766	791	-818	-1060	1183
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
54	-599	174	-567	-213	999	-25	864	-295	1471	128	659	-970	-765	594	-1140	-859	-779	50	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	7	8215	-9215	-732	-1329	-3111	-177	*	*											
55	-599	1398	984	-776	672	-433	-220	1563	-333	540	725	106	-765	402	-1140	-859	-779	-818	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
56	90	1074	133	-84	306	-433	-220	1641	270	-936	888	751	-765	-878	-1140	-75	-779	-818	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
57	-599	174	-984	-1157	-841	-433	-220	-129	876	-240	756	-258	-765	110	225	-859	-779	1474	-1060	1161
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
58	-599	1541	497	-1157	-841	-433	1060	-426	833	-936	753	-970	-765	-878	376	-859	1405	367	-1060	-902
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8215	9215	-732	-1329	-3111	-177	*	*											
59	1158	1541	-984	-1157	-841	-433	601	-238	661	-936	347	775	-765	-878	912	-578	156	-818	-1060	-902
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-	-7	-8215	-9215	-732	-1329	-3111	-177	*	*											
60	-599	174	34	-228	-841	-433	1586	-295	366	-240	924	-190	-765	332	-1140	-23	-779	-818	-1060	2174
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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61	-300	963	-315	-402	-1141	-733	308	1827	1169	-225	-1781	-1269	-69	-4	-985	-1159	-1078	-582	-1360	999
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8756	-9756	-732	-1329	-2548	-271	*	*											
62	-899	-125	1890	-1457	-1141	-57	-520	-1740	-667	-173	3033	-810	-1064	882	-215	-534	-1078	-1117	-1360	-1201

	206	979	178	352	36	372	585	-635	438	-130	677	-164	41	-73	335	54	27	-12	-255	97
	5	-8756	9756	732	1329	2548	-271	*	*											
63	241	1101	1283	1457	1141	733	-520	-536	-28	790	3158	-34	-1064	693	335	1159	-1078	-255	-1360	1201
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	73	335	-54	27	12	-255	97
	-5	-8756	9756	-732	-1329	2548	-271	*	*											
64	214	3570	-1283	1457	52	733	-520	-219	-28	-261	-1781	38	1364	103	-665	-337	-1078	-1117	-1360	-25
-	206	979	-178	-352	36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8756	9756	-732	1329	2548	-271	*	*											
65	-899	1159	1283	1457	479	-221	2319	-1416	480	-256	-532	-1269	504	-697	-1440	1743	-1078	-1117	-1360	-1201
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-	-5	-8756	-9756	-732	-1329	-2548	-271	*	*											
66	928	1559	-1283	-527	-1141	-733	801	-45	-222	-696	3191	-1269	-1064	758	-1440	-1159	-1078	-255	-1360	-1201
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67	-196	2696	-1283	-1457	-1141	-733	-520	-593	-667	-591	-1781	161	-1064	-1178	-1440	-1159	-496	1386	-1360	2644
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68	-314	620	1283	-1457	-51	1731	-520	-46	-112	-851	-1781	-34	-1064	1784	-1440	-565	-1078	-358	-1360	899
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-	-5	-8756	9756	-732	-1329	-2548	-271	*	*											
69	-899	-125	-1283	915	-653	-107	17	1915	-667	-539	803	-1269	-1064	-1178	-282	123	-258	135	-1360	-298
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-257	-8756	-2636	-732	-1329	-1152	-862	*	*											
70	-320	3550	-1303	-428	-510	381	854	-1760	-132	-1255	-1801	-1289	-1084	-1197	-255	300	1236	-154	-1379	431
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
71	7	1230	1303	-1477	1636	-470	540	-223	1891	-559	-1801	-338	-1084	-1197	-1460	-1179	-1098	735	1379	365
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
72	541	-145	-1303	-1477	-1161	-753	-540	-86	1662	-586	-65	-1289	-1084	-1197	-1005	-1179	-169	1708	-1379	1665
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8789	9789	-732	-1329	-2498	-281	*	*											
73	-439	542	162	-1477	60	-753	-540	-457	2048	-586	-459	-1289	-1084	-1197	1777	-894	-1098	-336	-1379	-1221
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	8789	-9789	-732	-1329	-2498	-281	*	*											
74	-919	1139	-1303	-810	-1161	-162	-540	-1760	685	-279	-1801	2157	-1084	-1197	-125	-342	-163	1267	-1379	-1221
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
75	-814	685	-1303	-428	-1161	-753	-540	1879	-132	846	-1801	-1289	-170	671	-1460	65	-1098	315	-1379	-1221
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
76	-919	-145	1951	-465	-198	-753	682	1385	-233	-3	-1801	-647	310	-448	-1460	-461	-431	-1137	-1379	-1221
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
77	-306	-145	-1303	307	-1161	-753	-540	-1760	1642	1604	-1801	-156	-1084	63	-243	-1179	-1098	-1137	-1379	-1221
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-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
78	-229	-145	-1303	1368	-1161	-753	683	-470	2047	-610	-1801	-82	-1084	-1197	-302	-553	-516	-316	-1379	-1221
-	206	979	-178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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79	919	-145	-284	1202	2307	-104	-540	-744	-687	-870	1801	309	-1084	-79	-255	-100	-233	-377	-1379	-1221
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-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
80	-919	-145	-251	1540	-17	-162	-540	-1760	1936	-945	-459	-1289	-841	-382	-899	-80	-1098	-474	-1379	248
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
81	-919	-145	1303	-48	-434	753	-540	1947	216	-363	-1801	-1289	-1084	63	53	-840	326	-1137	-1379	1933
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-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
82	-400	-145	1293	-498	947	-753	-540	2091	-687	-1255	-1801	-1289	-1084	-1197	634	-894	-516	-269	-1379	-1221
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-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
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-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
84	-234	-145	-61	-644	602	-753	-540	1298	185	-455	-1801	-748	-1084	1544	306	-1179	1017	-1137	-1379	-1221
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-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
85	711	-145	-451	-1477	-1161	-753	2362	1546	-687	-294	-1801	-159	-1084	55	-483	-357	-1098	-378	-1379	843
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-	-5	-8789	-9789	-732	-1329	-2498	-281	*	*											
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87	-585	-145	1303	-547	1713	-753	-540	-613	1577	-279	-1801	-571	-282	-1197	1348	-1082	9	1137	1379	161
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-	-265	-8789	-2597	-732	-1329	-2498	-281	*	*											
88	-351	622	1142	-1324	240	-600	698	86	573	-1102	-1649	-1136	100	-376	-1307	730	-945	320	1227	2294
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	12	255	97
-	-6	-8527	9527	-732	-1329	-2834	-218	*	*											
89	-248	7	1150	248	81	-600	-387	-1607	455	549	-1649	1718	-931	-1045	222	-1026	-945	-984	-1227	1811
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-6	-8527	-9527	-732	-1329	-2834	-218	*	*											
90	-766	7	-1150	467	-1008	80	-387	-1607	115	-1102	-1649	98	1272	-1045	72	1113	-615	968	-1227	-1069
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-154	-8527	-3347	-732	-1329	-2834	-218	*	*											
91	-51	89	-859	599	294	196	1392	-1032	282	-1021	-1567	-361	64	26	-1225	-944	296	1319	-1145	-987
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-120	-8379	-3698	-732	-1329	-2981	-195	*	*											
92	232	149	-1008	-366	1934	-458	-245	-1465	-392	-664	-1506	-355	-789	1139	656	-68	-803	41	-1085	657
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8263	-9263	-732	-1329	-3078	-182	*	*											
93	-26	1433	-42	-1182	-866	-458	-245	-1465	-392	-960	2588	-994	553	-159	40	-68	6	164	-1085	998
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8263	-9263	-732	-1329	-3078	-182	*	*											
94	-624	974	314	-1182	95	-232	37	-182	1082	-960	-1506	396	-789	2250	-1165	-168	-803	41	-1085	-927
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-7	-8263	-9263	-732	-1329	-3078	-182	*	*											
95	246	149	1008	-1182	-866	235	-245	-319	447	-960	-1506	-994	712	-903	1676	655	-531	-842	-1085	542
-	206	979	178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97

	-93	8263	-4076	732	-1329	1675	-542	*	*										
96	720	4	1154	348	752	603	-390	540	-537	811	1652	371	-336	1048	579	1029	1397	140	1230	1072
	206	979	178	352	-36	372	585	-635	438	130	-677	-164	41	-73	335	54	27	12	255	97
	-6	-8536	9536	-732	1329	-2851	-215	*	*										
97	111	4	1154	-718	1798	73	-390	-771	1605	496	-1652	-841	935	-438	1310	455	949	963	1230	1072
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	12	-255	-97
	-6	-8536	9536	-732	-1329	-2851	-215	*	*										
98	769	4	-1154	-429	727	-603	170	-1610	1680	-52	-1652	-1139	-935	-490	-1310	49	1387	361	-1230	-1072
	206	979	178	352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	65	-8536	4588	-732	-1329	-2851	-215	*	*										
99	-736	37	-1120	-1294	491	-570	-357	-560	197	-1072	-1618	1672	-901	-1015	1498	700	-124	-215	-1197	283
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	6	-8476	-9476	-732	-1329	-2917	-205	*	*										
100	-505	37	-1120	-1294	550	-570	-357	1430	51	-688	-1618	-29	-901	-1015	-78	-238	-915	1276	-1197	1313
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-76	-8476	4366	-732	-1329	-2917	-205	*	*										
101	6	76	-1082	-438	-939	-531	1046	-335	-145	1777	-1580	-284	-863	-976	-198	56	-877	-916	-1158	-1000
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-6	-8407	-9407	-732	-1329	-2986	-195	*	*										
102	698	76	-1082	12	-939	-531	-21	1494	-217	-46	-1580	-1068	-863	1870	-858	-384	-877	413	-1158	383
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-6	-8407	-9407	-732	-1329	-2986	-195	*	*										
103	-598	76	-1082	-438	150	145	-318	-335	1751	-1034	-1580	-1068	-863	-976	-602	-957	-877	364	-1158	2364
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	420	-8407	-2002	-732	-1329	-2986	-195	*	*										
104	487	286	-872	1498	244	305	-108	321	-255	87	645	-857	-652	-766	-1028	-747	666	-705	-948	1243
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	97
	-117	-7988	-3761	-732	-1329	-3275	-157	*	*										
105	-437	336	31	1547	-679	98	-58	600	-205	-530	252	-807	-603	750	-978	61	-617	-655	-898	-740
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-9	-7880	-8880	-732	-1329	-3334	-151	*	*										
106	-437	336	-822	1547	-679	-129	-58	-1278	598	-773	-1320	-807	-603	100	321	684	313	-655	-898	-740
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-9	-7880	-8880	-732	-1329	-3334	-151	*	*										
107	-437	336	-608	-84	543	-14	-58	-262	240	-164	-1320	-807	-603	-716	512	-403	-617	-655	-898	2429
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-9	-7880	-8880	-732	-1329	-3334	-151	*	*										
108	-437	336	1787	-357	-679	-154	1223	-262	832	-350	-1320	-807	-363	-716	-271	-697	-617	-655	-898	730
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-9	-7880	-8880	-732	-1329	-3334	-151	*	*										
109	-437	336	-822	-447	-679	-271	765	-1278	356	-773	-1320	401	-603	-319	-470	1452	489	563	-898	-740
	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
	-34	-7880	5714	-732	-1329	-3334	-151	*	*										
110	-426	347	-810	65	349	366	249	1634	-194	-762	-1308	281	-591	-705	-384	-686	309	-17	-887	-340
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	-9	-7858	-8858	-732	-1329	-3360	-148	*	*										
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-	206	979	-178	352	36	372	585	-635	438	-130	-677	-164	41	-73	335	54	27	-12	-255	-97
	634	-7858	1509	-732	1329	3360	-148	*	*											
113	178	595	-562	736	-420	12	201	604	54	93	-1060	-548	-343	661	719	186	507	466	-639	481
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-	-15	-7218	-8218	-732	-1329	-2162	-365	*	*											
114	-422	351	-807	-980	480	-256	-43	248	-190	-759	-1305	-793	445	116	-963	682	-70	23	-883	2663
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-106	-7851	-3904	-732	-1329	-3370	-147	*	*											
115	306	393	-764	-938	761	-214	351	-1221	418	-716	-1262	2036	-545	-659	-921	-640	-559	-205	-841	1159
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-77	-7755	-4407	-732	-1329	3414	-142	*	*											
116	334	422	-736	-910	509	-185	28	-1193	-120	-688	600	410	-517	-630	-892	1534	-531	-570	-812	742
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	11	-7688	-8688	-732	-1329	-3443	-139	*	*											
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	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	-12	255	97
	11	7688	-8688	-732	-1329	3443	-139	*	*											
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	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	54	27	12	255	97
	141	7688	-3506	-732	-1329	-3443	-139	*	*											
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	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-12	-7558	-8558	-732	-1329	-3492	-134	*	*											
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-	-12	-7558	-8558	-732	-1329	-3492	-134	*	*											
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-	-12	-7558	8558	-732	-1329	-3492	-134	*	*											
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127	-236	538	-620	-794	252	-70	143	-1077	-4	1551	-1118	-606	-401	-200	-776	-90	-109	-454	-696	-538
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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128	-236	538	-620	-794	233	-70	400	-1077	-4	-186	-1118	-182	-401	2338	-776	-496	-415	349	-696	-538
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	206	979	178	352	36	372	585	635	438	-130	677	-164	41	73	335	54	27	12	255	97
-	1279	-7250	783	732	1329	3590	-125	*	*											
130	143	917	-241	-415	99	309	522	-377	375	305	739	-227	-22	-135	-397	117	36	75	-317	159
-	206	979	-178	352	36	372	585	-635	438	-130	-677	-164	41	-73	335	-54	27	-12	-255	-97
-	-35	-5970	6970	-732	1329	3802	-107	*	*											
131	143	917	17	-415	99	309	522	-698	633	-193	-739	-227	-22	458	397	-117	-36	-75	-317	-159
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132	143	917	241	-415	-99	309	522	-698	375	-193	-739	-227	-22	-135	-397	-117	-36	-75	-317	1153
-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
-	*	*	*	*	*	*	*	*	*	0										

//

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ALPH  Amino
RF    no
CS    no
COM   [converted from an old Plan9 HMM]
NSEQ  0
DATE  Mon Mar  8 11:44:49 1999
XT      -8455     -4  -1000  -1000  -8455     -4  -8455     -4
NULT      -4  -8455
NULE     595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM        A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y

         m->m   m->i   m->d   i->m   i->i   d->m   d->d   b->m   m->e
        -3849      *   -104
     1  -1243   3362    377   -175  -1846    233   -224   -705  -1396  -1082  -1804    483   1754   -133   -496   -440   -411   -860  -2921  -1398
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -41 -15580  -5155   -732  -1329  -2028   -406  -3849      *
     2  -1097   4294    273   -591  -1829    190   -179   -883  -1847  -1201  -2130    848   -397    184  -1066   -631  -1083   -615  -1242  -1474
     -    179   1091   -143   -347    -57    372    595   -649    412   -146   -690   -126     62    -41   -333    -46      8    -37   -289   -109
     -  -7046    -33  -6071     -1 -11285  -2558   -268      *      *
     3  -1144   3490     86   -180  -1019    515   1204  -1205  -1645  -1856  -2683   1848   -622   -122   -240   -394   -507  -1185  -1847   -943
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -70 -15619  -4409   -732  -1329  -2833   -218      *      *
     4  -1063   2786       8   -549  -2315   1697    717  -1290  -1426  -1312  -1821    786    463    371     54   -346   -333  -1609  -3656   -913
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -75 -15588  -4307   -732  -1329  -1661   -549      *      *
     5   -469   3330   -240   -170  -1205   1710    261  -1770  -1747  -2058  -3115    949     19   -446  -1204   -369   -137  -1083  -1903  -1211
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -38 -15616  -5259   -732  -1329  -1892   -453      *      *
     6  -1119   3210   -349   -267  -1044    926    380   -898   -817  -1515  -1938      6    104    -71    259   -299    830   -260  -3057   -977
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -    -43 -15652  -5077   -732  -1329  -2136   -373      *      *
     7   -964   4380   -351   -862   -856    499   -143  -1459  -1531  -1602  -2239    347     19   -258   -649   -851   -426   -772  -2438   -885
     -    171   1104   -158   -342    -57    371    579   -611    409   -150   -695   -145     39    -63   -337    -57     49     -4   -285   -120
     -  -6428    -48  -5583     -1 -11338  -2576   -265      *      *
     8   -990   3659   1021   -321  -1011    417    186  -1494  -2082  -1748  -2137   1151    112   -169  -1273   -429    -50  -1151   -583   -263
     -    176   1058   -167   -354    -61    381    570   -640    413   -147   -688   -146     37    -43   -328    -55     71    -13   -276   -109
     -  -7242    -82  -4356     -1 -11119  -2505   -280      *      *
     9  -1143   3139    332    -61   -330    893    311  -1248  -1663  -1860  -2416   1004    521   -125   -763   -612     76   -444   -967    226
     -    206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
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```

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-	183	1177	-177	-348	-41	384	566	-635	405	-154	-702	-160	37	-67	-322	-60	22	-18	-280	-98
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-3	-15759	-8989	-732	-1329	-2777	-227	*	*											
13	-1081	3284	561	-56	-460	247	-189	-1946	-653	-858	-1334	415	1136	-133	-34	-447	-379	-1087	-866	-338
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-13	-15772	-6793	-732	-1329	-3241	-161	*	*											
14	-891	3432	-18	138	-594	670	-255	-1416	-1236	-1081	-2168	-81	1255	-137	-231	-243	-536	-1049	-541	-573
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16	-982	2474	-249	-331	1400	518	-128	-1885	-1581	-1597	-2819	-3	825	-215	-459	-111	-158	-1267	1490	1515
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17	-1194	3045	-626	-623	-142	1305	-466	-1360	-1123	-1969	-1569	-129	437	-229	-558	242	951	-993	-1611	201
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18	-1739	3160	-85	-512	385	1704	110	-950	-1468	-1290	-1591	117	22	-557	-290	-772	-641	-1302	-539	667
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-22	-15758	-6041	-732	-1329	-2994	-194	*	*											
19	-1505	2996	1200	50	-336	500	-227	-1495	-746	-1713	-2001	739	267	129	-488	-136	109	-1020	-1089	-58
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-15	-15750	-6608	-732	-1329	-1824	-479	*	*											
20	-1466	3206	653	-81	-373	611	424	338	-1976	-1172	-1731	291	-70	29	-704	-442	-206	-287	-1115	53
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-	-18	-15771	-6358	-732	-1329	-2437	-295	*	*											
21	-1490	3474	1466	-43	-623	623	-284	-1731	-1898	-1680	-1701	864	326	-207	-441	-708	-664	-1162	-1001	-440
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23	-1754	4079	414	-37	-528	470	-284	-2040	-1242	-1554	-1708	481	39	-134	-423	-297	-582	-2010	-645	-173
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24	-432	3192	-101	730	-1377	848	-150	-1770	-1118	-1253	-2102	95	793	278	-527	106	-164	-1494	-3057	-1136
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-	-76	-15724	-4279	-732	-1329	-2821	-220	*	*											
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26	-892	3343	44	-401	-1047	563	936	-1493	-1080	-1405	-1627	1051	810	-84	-26	69	-383	-1705	-1721	-926
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-	-59	-15562	-4637	-732	-1329	-3888	-101	*	*											
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29	-1887	3878	-387	-1015	-696	1151	277	-1750	-1677	-1954	-2729	1775	-847	-297	-548	-542	-578	-882	-3241	-1077
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-48	-15325	-4937	-732	-1329	-7009	-11	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-60	-15276	-4621	-732	-1329	-5491	-32	*	*											
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-	-38	-15226	-5266	-732	-1329	-5357	-36	*	*											
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-	-46	-15165	-4985	-732	-1329	-6625	-15	*	*											
37	-1425	3236	-757	-308	179	616	-162	-1595	-410	-2145	-1406	-909	-913	836	351	438	653	-972	-1305	648
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39	-1222	4855	-353	-703	-1200	374	-1228	-3007	-1704	-1542	-2708	-1191	472	-1185	-1402	-1310	-831	-2680	-353	-1431

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	40	-943	3598	-235	224	-358	1091	-408	-3062	-1616	-1481	-2952	-615	1581	-742	-1233	-412	-534	-1867	379	-202
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	-	-87	-14801	-4090	-732	-1329	-8563	-4	*	*											
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	-	-96	-14698	-3954	-732	-1329	-9247	-2	*	*											
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	-	-102	-14586	-3870	-732	-1329	-7202	-10	*	*											
	43	-1034	1293	-81	-979	-149	2152	225	-2316	-1452	-2646	-1340	-124	-903	-577	-1154	-121	1290	-1309	-1674	890
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	-	-101	-14488	-3885	-732	-1329	-9055	-3	*	*											
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	-	196	1001	-170	-346	-43	371	577	-641	437	-138	-685	-167	51	-68	-320	-49	37	-22	-271	-102
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	45	-2278	3752	515	-1715	-921	1515	780	-2365	-1664	-1011	-2693	668	-1542	-427	424	-679	77	-3386	-1821	-574
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	-	200	1010	-181	-357	-40	366	589	-641	432	-134	-682	-160	34	-73	-324	-39	33	-17	-259	-95
	-	-7524	-852	-1182	-9	-7395	-9794	-2	*	*											
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	-	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
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RF    no
CS    no
COM   [converted from an old Plan9 HMM]
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DATE  Mon Mar  8 11:45:02 1999
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NULT       -4  -8455
NULE      595  -1558     85    338   -294    453  -1158    197    249    902  -1085   -142    -21   -313     45    531    201    384  -1998   -644
HMM         A      C      D      E      F      G      H      I      K      L      M      N      P      Q      R      S      T      V      W      Y

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         -2869      *   -212
     1   -1711   -938    252  -2269    791   -530   1782  -2553   -255    400  -2594  -2082   1076  -1990    956    -58   -842   1319  -2172   -813
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -15  -9930  -6763   -732  -1329  -3342   -150  -2869      *
     2   -1680  -1012    444  -2343    337    794    659    -95    267     56     11  -2156    548  -2064   1150    410  -1787    360  -2246   -276
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -39 -10024  -5267   -732  -1329  -2044   -401      *      *
     3    -993  -1219  -2377  -2551      6     23    386    294    149    143  -2875  -2363   1471  -2271   2148    152  -2172     44  -2453  -2295
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -27 -10282  -5810   -732  -1329  -3178   -169      *      *
     4   -2026  -1252  -2410  -2584     40    495  -1646    738    506  -1034  -2908   -486   2035  -2304    -97    417   -783   1205  -2486  -2328
     -     206    979   -178   -352    -36    372    585   -635    438   -130   -677   -164     41    -73   -335    -54     27    -12   -255    -97
     -     -44 -10322  -5089   -732  -1329  -3734   -113      *      *
     5    -627  -1238  -2396  -1057   -206    477  -1632    420    377    197  -2894   -511   1099  -2290  -2552   -982    -66   1920  -2472  -2314
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     -     -66 -10305  -4502   -732  -1329  -3661   -119      *      *
     6   -1984  -1210   -662   -944   -500     22  -1604    375     63    558  -2866   -549    -36  -2262  -2524   -707    749   1923  -2444    223
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     -     -104 -10270  -3868   -732  -1329  -4011    -92      *      *
     7    -886  -1139    118  -2470   1076    866  -1533    249   -467   1467   -360  -2282    404  -2191  -2453   -165    181   -549  -2373  -2215
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     -     -29 -10181  -5714   -732  -1329  -2542   -272      *      *
     8    -905   -515   -840  -2578    692    629    469    825   -127    412    323  -2390    462  -2299  -1000    591   -568    976  -2481  -2323
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     -      -2 -10316 -11316   -732  -1329  -3192   -167      *      *
     9     417  -1297    570  -2629   -395   2129  -1692  -1011    -62   -869    271  -2441    922  -2350   -714    215  -2250   -233  -2532  -2373
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     -     -39 -10378  -5274   -732  -1329  -2733   -235      *      *
    10    -413  -1342   -319     84   -632    419   1786   -994    650   -553    224   -913   1755   -318   -454    410  -1245  -1116  -2576  -2418
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-	-92	-10432	-4028	-732	-1329	-2751	-232	*	*										
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-	-80	-10189	-4228	-732	-1329	-2560	-268	*	*										
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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14	58	710	127	1315	479	941	369	-731	939	-950	59	-627	-318	-629	-589	-1590	-431	-870	-2523	-2365
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15	-451	-1464	952	-271	-2479	-1144	-1858	-3078	-320	-410	83	-231	77	963	-143	-287	1449	803	-2698	389
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-	-88	-10681	-4088	-732	-1329	-2756	-231	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-61	-10628	-4613	-732	-1329	-1791	-492	*	*											
30	-2085	-1560	1339	-774	2034	104	1102	-339	-376	-2090	-231	-2704	-887	-482	265	-1212	457	-653	-2794	1724
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-44	-10692	-5087	-732	-1329	-3158	-171	*	*											
31	-1407	-1535	488	1228	752	-1133	-881	-3150	-1810	14	-3191	-2679	8	889	420	386	493	541	-2769	267
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-32	-10662	-5531	-732	-1329	-1976	-423	*	*											
32	-1206	737	-245	426	-2602	873	1673	295	338	-2170	-3242	-860	-2525	-418	1166	-46	781	-338	-2820	153
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-201	-10723	-2950	-732	-1329	-1997	-416	*	*											
33	451	-1007	-985	302	-774	-946	117	235	205	-2593	-3139	-2627	371	-2536	1181	627	1074	130	-2718	494
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-110	-10601	-3778	-732	-1329	-892	-1117	*	*											
34	-1996	68	-377	-969	-830	-188	1427	791	-25	-2742	102	-2776	120	996	-321	76	1047	1202	-2867	-572
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-30	-10777	-5624	-732	-1329	-1810	-484	*	*											
35	-698	-1667	-2825	-1534	-2683	-2275	482	52	-104	-2777	918	-2811	1688	-2720	601	1428	1104	-249	-2901	1130
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-209	-10817	-2895	-732	-1329	-2579	-264	*	*											
36	-2279	1479	-193	379	-2521	492	865	-967	-546	-2227	-3162	-2649	100	422	386	-71	1339	82	-2740	1719
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-126	-10628	-3596	-732	-1329	-1304	-749	*	*											
37	-2340	-1567	-729	-2898	-655	-2174	-265	794	-351	-720	-3222	-1051	435	-2619	1477	-292	2256	-1399	-2801	1236
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10700	-11700	-732	-1329	-2054	-398	*	*											
38	-554	-1629	-352	130	-758	-1248	-139	-982	774	-83	-251	-85	-76	-2681	793	-826	1955	-423	-2863	-577
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10773	-11773	-732	-1329	-3308	-154	*	*											
39	-1687	-1629	-361	-378	-822	-1310	-2024	-581	740	213	-3285	-2773	453	-539	2542	-190	-269	-634	-2863	-696
-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-1	-10773	-11773	-732	-1329	-1861	-465	*	*											
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-	206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
-	-85	-10839	-4147	-732	-1329	-2049	-399	*	*											
41	38	-1647	111	962	-2662	-685	27	-3261	-524	-1980	-2224	-632	1497	-1459	35	-584	955	853	-2881	1205